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(54) METHODS OF CREATING DWARF PHENOTYPES IN PLANTS

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(57) **ABSTRACT**

The invention is directed to the application of gene sequences which cause a dwarf phenotype in plants to the fields of forestry plants, ornamental horticultural plants, medicinal plants, and Nicotiana plants which are used for purposes other than for traditional tobacco products. The invention provides cDNAs identified by the polynucleotide sequences SEQ ID NO: 1-122 that may be used to create transfected or transgenic plants exhibiting a dwarf phenotype. The invention also provides methods of creating a transfected or transgenic plant exhibiting a dwarf phenotype by expressing in the plant DNA or mRNA identified by the sequences SEQ ID NO:1-122.

Figure 1a. GC/FID Conditions for the Analysis of Tobacco Metabolites in Fraction 1

Column: **Chrompack CPSil 8CB, 50 m x 0.32 mm i.d. with 0.25 micron film thickness**

Oven

Euilibration Time:	1 minute		
Initial Temperature:	50°C	Initial Time:	3.0 minutes

Ramps:	Rate (°C/min)	Final Temp(°C)	Final Time (min.)
#1	30	250	0.00
#2	25	340	5.50
#3	0		

Front and Back Inlet

Mode:	Split	Initial Temperature:	250°C
Pressure:	15 psig	Split Ratio:	5:1
Split Flow:	23.7 mL/min	Total Flow:	35.2 mL/min
Gas Saver:	Off	Gas:	Hydrogen
Mode:	Ramped pressure		
Initial Pressure: 15 psig		Initial Time:	0.0 minutes

Rate (psig/min)	Final Pres. (psig)	Final Time (min.)
5	40	10.0
10	50	3.0

Post Pressure:	15 psig		
Nominal Initial Flow:	4.7 mL/min	Average velocity:	68 cm/sec

Detector (Flame Ionization Detector; FID)

Temperature:	350°C	Hydrogen Flow:	40.0 mL/min
Air Flow:	400 mL/min	Mode:	Constant column flow
Makeup Flow:	25.0 mL/min	Makeup Gas Type:	Nitrogen
Electrometer:	On	Lit offset:	2.0
Flame:	On	Signal Data Rate:	10 Hz
Zero:	0	Range:	0
Fast Peaks:	Off	Attenuation:	0

APEX Injector

Injector Mode Program

	Mode	Front Minutes	Back Minutes
Initial	GC Split	0.00	0.00
1	Splitless	0.20	1.25
2	Prosep Split	4.00	6.00
3	GC Split	6.00	8.00

Precolumn Temperature Program

Rate (C/min)	Target (C)	Front Minutes	Back Minutes
	50	0.20	1.25
300	400	10.00	10.00

Figure 1b. GC/FID Conditions for the Analysis of Tobacco Metabolites in Fraction 2

Liners:	**Restek split/splitless single-taper liner 4 mm i.d (borosilicate) without silanized glass wool.**		
Column:	**DB23 from J & W, 15 m x 0.25 mm i.d. with 0.15 micron film thickness**		
Oven			
Equilibration Time:	0.1 minute		
Initial Temperature:	70°C	Initial Time:	2.0 minutes

Ramps:	Rate (°C/min)	Final Temp(°C)	Final Time (min.)
#1	25	170	0.00
#2	10	220	1.00

Dual injection mode:	Start program with front injection.		
Front Inlet			
Mode:	Splitless	Temperature:	230°C
Pressure:	12.9 psi	Spliless: NA	
Split vent	time: 1.00 min	Flow: 35 mL/min	
Gas Saver:	On (5 minutes)	Flow: 20 mL/min	
Gas:	Helium		
Mode:	2 ml/min constant flow		
Total Flow:	24.5 mL/min	Average velocity: 53 cm/sec	
Back Inlet			
Mode:	Splitless	Temperature:	230°C
Pressure:	12.9 psi	Spliless: NA	
Split vent	time: 2.00 min	Flow: 35 mL/min	
Gas Saver:	On (5 minutes)	Flow: 20 mL/min	
Gas:	Helium		
Mode:	2 ml/min constant flow		
Total Flow:	24.5 mL/min	Average velocity: 53 cm/sec	
Detectors (Flame Ionization Detector; FID)			
Temperature:	240°C	Hydrogen Flow:	40.0 mL/min
Air Flow:	400 mL/min	Mode:	Constant column flow
Makeup Flow:	25.0 mL/min	Makeup Gas Type:	Nitrogen
Electrometer:	On	Lit offset:	2.0
Flame:	On	Signal Data Rate:	10 Hz
Zero:	0	Range:	0
Fast Peaks:	Off	Attenuation:	0

Fraction 3

Figure 1c. GC/FID Conditions for the Analysis of Tobacco Metabolites in Fraction 3

Column:	**Chrompack CPSil 8CB, 50 m x 0.32 mm i.d. with 0.25 micron film thickness**			
Oven				
Euilibration Time:	1 minute			
Initial Temperature:	50°C		Initial Time:	2.0 minutes

Ramps:	Rate (°C/min)	Final Temp(°C)	Final Time (min.)
#1	30	250	0.00
#2	25	325	3.00
#3	0		

Front and Back Inlet			
Mode:	Split	Initial Temperature:	290°C
Pressure:	15 psig	Split Ratio:	5:1
Split Flow:	23.7 mL/min	Total Flow:	35.2 mL/min
Gas Saver:	Off	Gas:	Hydrogen
Mode:	Ramped pressure		
Initial Pressure: 15 psig		Initial Time:	1.0 minutes

Rate (psig/min)	Final Pres. (psig)	Final Time (min.)
5	40	10.0
10	50	3.0

Post Pressure:	15 psig		
Nominal Initial Flow:	4.7 mL/min	Average velocity:	68 cm/sec
Detector (Flame Ionization Detector: FID)			
Temperature:	350°C	Hydrogen Flow:	40.0 mL/min
Air Flow:	400 mL/min	Mode:	Constant
column+makeup Combined Flow:	20 mL/min	Makeup Flow:	25.0 mL/min
Makeup Gas Type:	Nitrogen		
Electrometer:	On	Lit offset:	2.0
Flame:	On	Signal Data Rate:	20 Hz
Zero:	0	Range:	0
Fast Peaks:	Off	Attenuation:	0

APEX Injector

Inj Volume: 2.5 ul

Injector Mode Program

	Mode	Front Minutes	Back Minutes
Initial	GC Split	0.00	0.00
1	Splitless	0.00	0.00
3	GC Split	5.00	5.00

Precolumn Temperature Program

Rate (C/min)	Target (C)	Front Minutes	Back Minutes
	100	0.87	0.87
300	325	10.00	10.00

Figure 1d. LC/FLD Parameters for the Analysis of Tobacco Metabolites in Fraction 4

Column:	Aminoquant Hypersil ODS 5-µm column (200 mm x 2.1 mm)
Guard Column:	Hypersil ODS 5 µm (20 mm x 2.1 mm)
Column Temperature:	45 °C

Agilent 1100 Binary Pump Program

Mobile Phase A:	Aqueous Acetate Buffer pH7.2 containing EDTA (4ug/mL), triethylamine (0.18uL/mL), THF (0.3%) (v:v)
Mobile Phase B:	Aqueous Acetate Buffer pH7.2:methanol:acetonitrile (2:4:4) (v:v:v)

Pump Program

Time (min)	% B	Flow (mL)
0.0	0	0.6
9.5	60	0.6
10	100	0.6
10.5	100	1.1
13.1	100	0.6
14	0	0.6

Agilent 1100 Autosampler Program

Step 1. Draw 5 uL borate buffer
Step 2. Draw 1 uL OPA reagent
Step 3. Draw 0 uL water (Needle Wash)
Step 4. Draw 1 uL sample
Step 5. Mix 7 uL air 5 times
Step 6. Draw 0 uL water (Needle Wash)
Step 7. Draw 1 uL FMOC reagent
Step 8. Draw 0 uL water (Needle Wash)
Step 9. Draw 1 uL borate buffer
Step 10. Mix 9 uL air 3 times
Step 11. Inject

Agilent 1100 Fluorescent Detector

Time 0.0	
Excitation:	340 nm
Emission:	450 nm
PMT Gain:	10
Time 9.2 min	
Excitation:	266 nm
Emission:	305 nm
PMT Gain:	9

METHODS OF CREATING DWARF PHENOTYPES IN PLANTS

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims the priority benefit of provisional U.S. Patent Application Serial No. 60/219,943, filed Jul. 20, 2000, which is hereby incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] This invention relates to nucleic acids and amino acid sequences identified in multiple metabolic pathways that lead to dwarfism and stunting in plants and the use of these sequences to create dwarf varieties of any plant species. Particularly, this invention relates to the use of nucleic acids and amino acid sequences which cause dwarfing in the fields of forestry plants, ornamental horticultural plants, medicinal plants, and Nicotiana plants.

BACKGROUND OF THE INVENTION

[0003] The strategies for increasing the productivity of plants is dependent on rapid discovery of unknown gene sequences and their function through genomics research. These discoveries will provide fundamental information necessary to engineer plants for improved grain yields and resistance to drought, pests, salt, and other extreme environmental conditions. Such advances are critical for a world population expected to double by 2050. Moreover, this information may identify genes and products encoded by genes that are useful for human and animal healthcare such as pharmaceuticals.

[0004] There has been a massive accumulation of expressed sequence tags (ESTs) as a result of recent genome research. Potential use of this sequence information is enormous once gene function is determined. Knowledge of function allows engineering of commercial plants and seeds for forestry, ornamental and horticultural plants, including any plants used to produce pharmaceutical products, and particularly plants of the genus Nicotiana for purposes other than traditional tobacco products.

[0005] Use of these sequences to convey any number of desirable traits to pharmaceutical and fiber crops and thereby increase production and building materials, medicines and chemicals for other uses. For example, gene profiling in cottonwood may lead to an understanding of the types of genes and promoters that act primarily in fiber cells. The novel sequences derived from these profiling studies may be important in genetic engineering of cottonwood fiber for increased strength. In plant breeding, gene profiling coupled to physiological trait analysis can lead to the identification of predictive markers that will be increasingly important in marker assisted breeding programs. Mining the DNA sequence of a particular crop for genes important for yield, quality, health, appearance, color, taste, etc. are applications of obvious importance for crop improvement.

[0006] The Green Revolution crops, introduced in the late 1960s and early 1970s, produce several times as much grain as the traditional varieties they replaced, and they spread rapidly. They enabled India to double its wheat crop in seven years, dramatically increasing food supplies and averting widely predicted famine. The Green Revolution's leading research achievement was to hasten the perfection of dwarf spring wheat. Though it is conventionally assumed that farmers want a tall, impressive-looking harvest, in fact shrinking wheat and other crops has often proved beneficial. When bred for short stalks, plants expend less energy growing inedible column sections and more growing valuable grain. Stout, short-stalked wheat also neatly supports its kernels, whereas tall-stalked wheat may bend over at maturity, complicating reaping. Nature has favored genes for tall stalks, because in nature plants must compete for access to sunlight. However, in high-yield agriculture, equally short-stalked plants will receive equal sunlight. Researchers are actively seeking dwarf strains of rice and other crops in order to increase agronomic yields. The identification of genes and metabolic pathways that may be modified to create rapidly growing dwarf strains would greatly accelerate this effort. Furthermore, identification of these genes and metabolic pathways in food crops may lead to the development of dwarf strains in other plant types such as forest trees, ornamental species such as ornamental and turfgrass, and plants such as Nicotiana sp. grown as hosts for biopharmaceutical manufacturing.

SUMMARY OF THE INVENTION

[0007] The invention is directed to the application of gene sequences which cause a dwarf phenotype in plants to the fields of forestry plants, ornamental horticultural plants, medicinal plants, and Nicotiana plants which are used for purposes other than for traditional tobacco products.

[0008] The invention provides cDNAs identified by the polynucleotide sequences SEQ ID NO: 1-122 that may be used to create transfected or transgenic plants exhibiting a dwarf phenotype. These cDNAs have been identified by phenotypic screening of the Large Scale Biology's libraries over 8000 cDNAs from Arabidopsis, Nicotiana, Oryza and Papaver constructed in the GENEWARE® vector.

[0009] The invention provides methods of creating a transfected or transgenic plant exhibiting a dwarf phenotype comprising: expressing in the plant a cDNA (or its encoded mRNA) identified by a polynucleotide sequence chosen from the group consisting of SEQ ID NO: 1-122.

[0010] The invention also provides a method of creating a transfected or transgenic plant exhibiting a dwarf phenotype comprising the steps of: (a) providing a viral inoculum capable of infecting a plant comprising the cDNA (or its encoded mRNA) identified by a polynucleotide sequence chosen from the group of SEQ ID NO: 1-122; and (b) applying said viral inoculum to a plant; whereby the plant is infected and the cDNA (or its encoded mRNA) is expressed in the plant.

[0011] The methods of the invention provide for creating a transfected or transgenic plant exhibiting a dwarf phenotype in any plant type. Preferred embodiments of the invention provide methods for creating dwarf plants of ornamental and horticultural plants, medicinal plants or forest trees. A preferred embodiment provides methods for creating dwarf plants of Nicotiana sp. Another preferred embodiment provides methods for creating dwarf turfgrass.

[0012] The invention also provides methods for creating transfected or transgenic plants exhibiting a dwarf pheno-

type for use in biopharmaceutical manufacturing comprising: applying a viral inoculum capable of infecting a plant and comprising the DNA (or its encoded mRNA) identified by a polynucleotide sequence chosen from the group of SEQ. ID NO 1-122 to a plant that expresses a biopharmaceutical, whereby the plant is infected, exhibits a dwarf phenotype, and expresses the biopharmaceutical.

[0013] The invention also provides a transfected or transgenic plant exhibiting a dwarf phenotype made by the method comprising expressing in the plant a cDNA(or its encoded mRNA) identified by a polynucleotide sequence chosen from the group consisting of SEQ ID NO: 1-122. The invention provides for transfected or transgenic plants made by the use of this method with any plant type. Preferred embodiments are transfected or transgenic plants of ornamental and horticultural plants, medicinal plants or forest trees. Preferred embodiments include transfected or transgenic plants of Nicotiana sp and dwarf turfgrass.

[0014] The invention also provides methods of producing multiple crops of the transfected or transgenic plants expressing a cDNA(or its encoded mRNA) identified by a polynucleotide sequence chosen from the group consisting of SEQ ID NO: 1-122 and exhibiting a dwarf phenotype comprising the steps of: (a) planting a reproductive unit of the transfected or transgenic plant; (b) growing the planted reproductive unit under natural light conditions; (c) harvesting the plant; and (d) repeating steps (a) through (c) at least once in the year.

[0015] The invention provides a method of constructing and characterizing a normalized cDNA library in a viral vector. The invention further provides a method of constructing and characterizing of a normalized whole plant cDNA library in viral vectors.

[0016] The invention identifies cDNAs corresponding to genes in the trans-ketolase and carbohydrate metabolic pathways as useful for creating transfected or transgenic plants exhibiting a dwarf phenotype.

[0017] The invention also provides method of manufacturing a biopharmaceutical comprising:

DESCRIPTION OF THE INVENTION

[0018] Before the present proteins, nucleotide sequences, and methods are described, it should be noted that this invention is not limited to the particular methodology, protocols, plants, cell lines, vectors, and reagents described herein as these may vary. It should also be understood that the terminology used herein is for the purpose of describing particular aspects of the invention, and is not intended to limit its scope which will be limited only by the appended claims.

[0019] It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a host cell" includes a plurality of such host cells, reference to the "antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

[0020] Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are reported in the publications which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

[0021] "Acylate" as used herein, refers to the introduction of an acyl group into into a molecule, i.e. acylation

[0022] "Adjacent" as used herein, refers to a position in a nucleotide sequence proximate to and 5' or 3' to a defined sequence. Generally, adjacent means within 2 or 3 nucleotides of the site of reference.

[0023] "Agonist", as used herein, refers to a molecule which, when bound to a gene product of interest, increases the biological or immunological activity of that gene product. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to a gene product of interest.

[0024] "Alterations" in a polynucleotide sequence, as used herein, comprise any deletions, insertions, and point mutations in the polynucleotide sequence. Included within this definition are alterations to any genomic DNA sequence corresponding to the polynucleotide sequence.

[0025] "Amino acid sequence" as used herein refers to an oligopeptide, peptide, polypeptide, or protein sequence, and fragments or portions thereof, and to naturally occurring or synthetic molecules. "Amino acid sequence" and like terms, such as "polypeptide" or "protein" as recited herein are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

[0026] "Amplification" as used herein refers to the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction (PCR) technologies well known in the art (Dieffenbach, C. W. and G. S. Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y.).

[0027] "Antibody" refers to intact molecules as well as fragments thereof which are capable of specific binding to the epitopic determinant. Antibodies that bind a polypeptide of interest can be prepared using intact polypeptides or fragments as the immunizing antigen. These antigens may be conjugated to a carrier protein, if desired.

[0028] "Antigenic determinant,""determinant group," or "epitope of an antigenic macromolecule" as used herein, refers to any region of the macromolecule with the ability or potential to elicit, and combine with, specific antibody. Determinants exposed on the surface of the macromolecule are likely to be immunodomi-

nant, i.e. more immunogenic than other (imunorecessive) determinants which are less exposed, while some (e.g. those within the molecule) are non-immunogenic (immunosilent). As used herein, antigenic determinant refers to that portion of a molecule that makes contact with a particular antibody (i.e., an epitope). When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

[0029] "Antisense", as used herein, refers to nucleotide sequences which are complementary to a specific DNA or RNA sequence. The term "antisense" or "(−) sense" is used in reference to the nucleic acid strand that is complementary to the "sense" or "(+) sense" strand. The designation "negative" is sometimes used in reference to the antisense strand, and "positive" is sometimes used in reference to the sense strand. Antisense molecules may be produced by any method, including synthesis by ligating the gene of interest in a reverse orientation to a viral promoter which permits the synthesis of a complementary strand. Once introduced into a cell, the transcript of this strand may hybridize to natural sequences to block either their further transcription or translation. In this manner, mutant phenotypes may be generated.

[0030] "Anti-Sense Inhibition" as used herein, refers to a type of gene regulation based on cytoplasmic, nuclear or organelle inhibition of gene expression due to the presence in a cell of an RNA molecule complementary to at least a portion of the mRNA being translated. It is specifically contemplated that DNA molecules may be from either an RNA virus or mRNA from the host cells genome or from a DNA virus.

[0031] "Antagonist" or "inhibitor", as used herein, refer to a molecule which, when bound to a gene product of interest, decreases the biological or immunological activity of that gene product of interest. Antagonists and inhibitors may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to the gene product of interest.

[0032] "Biologically active", as used herein, refers to a molecule having the structural, regulatory, or biochemical functions of a naturally occurring molecule.

[0033] "Cell Culture" as used herein, refers to a proliferating mass of cells which may be in either an undifferentiated or differentiated state, growing contiguously or non-contiguously.

[0034] "Chimeric plasmid" as used herein, refers to any recombinant plasmid formed (by cloning techniques) from nucleic acids derived from organisms which do not normally exchange genetic information (e.g. *Escherichia coli* and *Saccharomyces cerevisiae*).

[0035] "Chimeric Sequence" or "Chimeric Gene" as used herein, refers to a nucleotide sequence derived from at least two heterologous parts. The sequence may comprise DNA or RNA.

[0036] "Coding Sequence" as used herein, refers to a nucleic acid sequence which, when transcribed and translated, results in the formation of a cellular polypeptide or a ribonucleotide sequence which, when translated, results in the formation of a cellular polypeptide.

[0037] "Common Embryological Basis" as used herein, is intended to include all tissues which are derived from the same germinal layer, specifically the ectoderm layer, which forms during the gastrulation stage of embryogenesis. Such tissues include, but are not limited to, brain, epithelium, adrenal medulla, spinal chord, retina, ganglia and the like.

[0038] "Compatible" as used herein, refers to the capability of operating with other components of a system. A vector or plant viral nucleic acid which is compatible with a host is one which is capable of replicating in that host. A coat protein which is compatible with a viral nucleotide sequence is one capable of encapsidating that viral sequence.

[0039] "Complementary" or "Complementarity", as used herein, refer to the Watson-Crick base-pairing of two nucleic acid sequences. For example, for the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two nucleic acid sequences may be "partial", in which only some of the bases bind to their complement, or it may be complete as when every base in the sequence binds to it complementary base. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands.

[0040] "Complementation analysis" as used herein, refers to observing the changes produced in an organism when a nucleic acid sequence is introduced into that organism after a selected gene has been deleted or mutated so that it no longer functions fully in its normal role. A complementary gene to the deleted or mutated gene can restore the genetic phenotype of the selected gene.

[0041] "Constitutive expression" as used herein refers to gene expression which features substantially constant or regularly cyclical gene transcription. Generally, genes which are constitutively expressed are substantially free of induction from an external stimulus.

[0042] "Correlates with expression of a polynucleotide", as used herein, indicates that the detection of the presence of ribonucleic acid that is similar to and indicative of the presence of an mRNA encoding a polypeptide in a sample and thereby correlates with expression of the transcript from the polynucleotide encoding the protein.

[0043] "Deletion", as used herein, refers to a change made in either an amino acid or nucleotide sequence resulting in the absence one or more amino acids or nucleotides, respectively.

[0044] "Differentiated cell" as used herein refers to a cell which has substantially matured to perform one or more biochemical or physiological functions.

[0045] "Dwarf Plant" as used herein, refers to a plant that is much below the height or size of its kind or related species.

[0046] "Encapsidation" as used herein, refers to the process during virion assembly in which nucleic acid becomes incorporated in the viral capsid or in a head/capsid precursor (e.g. in certain bacteriophages).

[0047] "Exon" as used herein, refers to a polynucleotide sequence in a nucleic acid that codes information for protein synthesis and that is copied and spliced together with other such sequences to form messenger RNA.

[0048] "Expression" as used herein is meant to incorporate one or more of transcription, reverse transcription and translation.

[0049] "Expressed sequence tag (EST)" as used herein refers to relatively short single-pass DNA sequences obtained from one or more ends of cDNA clones and RNA derived therefrom. They may be present in either the 5' or the 3' orientation. ESTs have been shown useful for identifying particular genes.

[0050] "Foreign gene" as used herein, refers to any sequence that is not native to the virus.

[0051] "Fusion protein" as used herein, refers to a protein containing amino acid sequences from each of two distinct proteins; it is formed by the expression of a recombinant gene in which two coding sequences have been joined together such that their reading frames are in phase. Hybrid genes of this type may be constructed in vitro in order to label the product of a particular gene with a protein which can be more readily assayed (e.g. a gene fused with lacZ in *E. coli* to obtain a fusion protein with β-galactosidase activity). Alternatively, a protein may be linked to a signal peptide to allow its secretion by the cell. The products of certain viral oncogenes are fusion proteins.

[0052] "Gene" as used herein, refers to a discrete nucleic acid sequence responsible for a discrete cellular product and/or performing one or more intercellular or intracellular functions. The term "gene", as used herein, refers not only to the nucleotide sequence encoding a specific protein, but also to any adjacent 5' and 3' non-coding nucleotide sequence involved in the regulation of expression of the protein encoded by the gene of interest. These non-coding sequences include terminator sequences, promoter sequences, upstream activator sequences, regulatory protein binding sequences, and the like. These non-coding sequence gene regions may be readily identified by comparison with previously identified eukaryotic non-coding sequence gene regions. Furthermore, the person of average skill in the art of molecular biology is able to identify the nucleotide sequences forming the non-coding regions of a gene using well-known techniques such as a site-directed mutagenesis, sequential deletion, promoter probe vectors, and the like.

[0053] "Growth cycle" as used herein is meant to include the replication of a nucleus, an organelle, a cell, or an organism.

[0054] "Half-life" as used herein, refers to the time required for half of something to undergo a process (e.g. the time required for half the amount of a substance, such as a drug or radioactive tracer, in or introduced into a living system or ecosystem to be eliminated or disintegrated by natural processes.

[0055] "Heterologous" as used herein, refers to the association of a molecular or genetic element associated with a distinctly different type of molecular or genetic element.

[0056] "Host" as used herein, refers to a cell, tissue or organism capable of replicating a vector or plant viral nucleic acid and which is capable of being infected by a virus containing the viral vector or plant viral nucleic acid. This term is intended to include procaryotic and eukaryotic cells, organs, tissues or organisms, where appropriate.

[0057] "Homology" as used herein, refers to the degree of similarity between two or more nucleotide or amino-acid sequences. Homology may be partial or complete.

[0058] "Hybridization", as used herein, refers to any process by which a strand of nucleic acid binds with a complementary or partially complementary strand through base pairing.

[0059] "Hybridization complex", as used herein, refers to a complex formed between nucleic acid strands by virtue of hydrogen bonding, stacking or other non-covalent interactions between bases. A hybridization complex may be formed in solution or between nucleic acid sequences present in solution and nucleic acid sequences immobilized on a solid support (e.g., membranes, filters, chips, pins or glass slides to which cells have been fixed for in situ hybridization).

[0060] "Immunologically active" refers to the capability of a natural, recombinant, or synthetic gene product of interest, or any oligopeptide thereof, to bind with specific antibodies and induce a specific immune response in appropriate animals or cells.

[0061] "Induction" and the terms "induce", "induction" and "inducible" as used herein, refer generally to a gene and a promoter operably linked thereto which is in some manner dependent upon an external stimulus, such as a molecule, in order to actively transcribed and/or translate the gene.

[0062] "Infection" as used herein refers to the ability of a virus to transfer its nucleic acid to a host or introduce a viral nucleic acid into a host, wherein the viral nucleic acid is replicated, viral proteins are synthesized, and new viral particles assembled. In this context, the terms "transmissible" and "infective" are used interchangeably herein. The term is also meant to include the ability of a selected nucleic acid sequence to integrate into a genome, chromosome or gene of a target organism.

[0063] "Insertion" or "Addition", as used herein, refers to the replacement or addition of one or more nucleotides or amino acids, to a nucleotide or amino acid sequence, respectively.

[0064] "In cis" as used herein, indicates that two sequences are positioned on the same strand of RNA or DNA.

[0065] "In trans" as used herein, indicates that two sequences are positioned on different strands of RNA or DNA.

[0066] "Intron" as used herein refers to a polynucleotide sequence in a nucleic acid that does not code information for protein synthesis and is removed before translation of messenger RNA.

[0067] "Isolated" as used herein refers to a polypeptide, polynucleotide molecules separated not only from other peptides, DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule but also from other macromolecules and preferably refers to a macromolecule found in the presence of (if anything) only a solvent, buffer, ion or other component normally present in a solution of the same. "Isolated" and "purified" do not encompass either natural materials in their native state or natural materials that have been separated into components (e.g., in an acrylamide gel) but not obtained either as pure substances or as solutions.

[0068] "Kinase" as used herein, refers to an enzyme (e.g. hexokinase and pyruvate kinase) which catalyzes the transfer of a phosphate group from one substrate (commonly ATP) to another.

[0069] "Marker" or "Genetic Marker" as used herein, refers to a genetic locus which is associated with a particular, usually readily detectable, genotype or phenotypic characteristic (e.g., an antibiotic resistance gene).

[0070] "Metabolome" as used herein, indicates the complement of relatively low molecular weight molecules that is present in a plant, plant part, or plant sample, or in a suspension or extract thereof. Examples of such molecules include, but are not limited to: acids and related compounds; mono-, di-,and tri-carboxylic acids (saturated, unsaturated, aliphatic and cyclic, aryl, alkaryl); aldo-acids, keto-acids; lactone forms; gibberellins; abscisic acid; alcohols, polyols, derivatives, and related compounds; ethyl alcohol, benzyl alcohol, menthanol; propylene glycol, glycerol, phytol; inositol, furfuryl alcohol, menthol; aldehydes, ketones, quinones, derivatives, and related compounds; acetaldehyde, butyraldehyde, benzaldehyde, acrolein, furfural, glyoxal; acetone, butanone; anthraquinone; carbohydrates; mono-, di-, tri-saccharides; alkaloids, amines, and other bases; pyridines (including nicotinic acid, nicotinamide); pyrimidines (including cytidine, thymine); purines (including guanine, adenine, xanthines/hypoxanthines, kinetin); pyrroles; quinolines (including isoquinolines); morphinans, tropanes, cinchonans; nucleotides, oligonucleotides, derivatives, and related compounds; guanosine, cytosine, adenosine, thymidine, inosine; amino acids, oligopeptides, derivatives, and related compounds; esters; phenols and related compounds; heterocyclic compounds and derivatives; pyrroles, tetrapyrroles (corrinoids and porphines/porphyrins, w/w/o metal-ion); flavonoids; indoles; lipids (including fatty acids and triglycerides), derivatives, and related compounds; carotenoids, phytoene; and sterols, isoprenoids including terpenes.

[0071] "Modulate" as used herein, refers to a change or an alteration in the biological activity of a gene product of interest. Modulation may be an increase or a decrease in protein activity, a change in binding characteristics, or any other change in the biological, functional or immunological properties of the gene product of interest.

[0072] "Movement protein" as used herein refers to a noncapsid protein required for cell to cell movement of replicons or viruses in plants.

[0073] "Multigene family" as used herein refers to a set of genes descended by duplication and variation from some ancestral gene. Such genes may be clustered together on the same chromosome or dispersed on different chromosomes. Examples of multigene families include those which encode the histones, hemoglobins, immunoglobulins, histocompatibility antigens, actins, tubulins, keratins, collagens, heat shock proteins, salivary glue proteins, chorion proteins, cuticle proteins, yolk proteins, and phaseolins.

[0074] "Non-Native" as used herein refers to any RNA or DNA sequence that does not normally occur in the cell or organism in which it is placed. Examples include recombinant plant viral nucleic acids and genes or ESTs contained therein. That is, a RNA or DNA sequence may be non-native with respect to a viral nucleic acid. Such a RNA or DNA sequence would not naturally occur in the viral nucleic acid. Also, a RNA or DNA sequence may be non-native with repect to a host organism. That is, such a RNA or DNA sequence would not naturally occur in the host organism. Conversely, the term non-native does not imply that a RNA or DNA sequence must be non-native with respect to both a viral nucleic acid and a host organism concurrently. The present invention specifically contemplates placing a RNA or DNA sequence which is native to a host organism into a viral nucleic acid in which it is non-native.

[0075] "Nucleic acid sequence" as used herein refers to a polymer of nucleotides in which the 3' position of one nucleotide sugar is linked to the 5' position of the next by a phosphodiester bridge. In a linear nucleic acid strand, one end typically has a free 5' phosphate group, the other a free 3' hydroxyl group. Nucleic acid sequences may be used herein to refer to oligonucleotides, or polynucleotides, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand. The term is intended to encompass all nucleic acids whether naturally occurring in a particular cell or organism or non-naturally occurring in a particular cell or organism.

[0076] "Operably Linked" refers to a juxtaposition of components, particularly nucleotide sequences, such that the normal function of the components can be performed. Thus, a coding sequence that is operably linked to regulatory sequences refers to a configuration of nucleotide sequences wherein the coding sequences can be expressed under the regulatory control i.e., transcriptional and/or translational control, of the regulatory sequences.

[0077] "Organism" and "host organism" as used herein is specifically intended to include animals (including humans), plants, viruses, fungi, and bacteria.

[0078] "Origin of Assembly" as used herein, refers to a sequence where self-assembly of the viral RNA and the viral capsid protein initiates to form virions.

[0079] "Outlier Peak" as used herein, indicates a peak of a chromatogram of a test sample, or the relative or absolute detected response data, or amount or concentration data thereof. An outlier peak: 1) may have a significantly different peak height or area as compared to a like chromatogram of a control sample; or 2) be an additional or missing peak as compared to a like chromatogram of a control sample.

[0080] "Phenotype" or "Phenotypic Trait(s)" as used herein, refers to an observable property or set of properties resulting from the expression or suppression of a gene or genes.

[0081] "Plant" as used herein refers to any plant and progeny thereof, and to parts of plants including parts of plants, including seed, cuttings, tubers, fruit, flowers, branches, leaves, plant cells and other parts of any tree or other plant used in forestry, ornamental horticultural plants, medicinal plants including any plants used to produce pharmaceutical products, and plants of the genus Nicotiana which are used for purposes other than for traditional tobacco products.

[0082] "Plant Cell" as used herein, refers to the structural and physiological unit of plants, consisting of a protoplast and the cell wall.

[0083] "Plant Organ" as used herein, refers to a distinct and visibly differentiated part of a plant, such as root, stem, leaf or embryo.

[0084] "Plant Tissue" as used herein, refers to any tissue of a plant in planta or in culture. This term is intended to include a whole plant, plant cell, plant organ, protoplast, cell culture, or any group of plant cells organized into a structural and functional unit.

[0085] "Portion" as used herein, with regard to a protein (i.e. "a portion of a given protein") refers to fragments of that protein. The fragments may range in size from four amino acid residues to the entire amino acid sequence minus one amino acid.

[0086] "Positive-sense inhibition" as used herein refers to a type of gene regulation based on cytoplasmic inhibition of gene expression due to the presence in a cell of an RNA molecule substantially homologous to at least a portion of the mRNA being translated.

[0087] "Production Cell" as used herein, refers to a cell, tissue or organism capable of replicating a vector or a viral vector, but which is not necessarily a host to the virus. This term is intended to include prokaryotic and eukaryotic cells, organs, tissues or organisms, such as bacteria, yeast, fungus and plant tissue.

[0088] "Promoter" as used herein, refers to the 5'-flanking, non-coding sequence substantially adjacent a coding sequence which is involved in the initiation of transcription of the coding sequence.

[0089] "Protoplast" as used herein, refers to an isolated plant cell without cell walls, having the potency for regeneration into cell culture or a whole plant.

[0090] "Purified" as used herein when referring to a peptide or nucleotide sequence, indicates that the molecule is present in the substantial absence of other biological macromolecular, e.g., polypeptides, polynucleic acids, and the like of the same type. The term "purified" as used herein preferably means at least 95% by weight, more preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above.

[0091] "Substantially purified" as used herein, refers to nucleic or amino acid sequences that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated.

[0092] "Recombinant Plant Viral Nucleic Acid" as used herein, refers to a plant viral nucleic acid which has been modified to contain non-native nucleic acid sequences. These non-native nucleic acid sequences may be from any organism or purely synthetic, however, they may also include nucleic acid sequences naturally occurring in the organism into which the recombinant plant viral nucleic acid is to be introduced.

[0093] "Recombinant Plant Virus" as used herein, refers to a plant virus containing a recombinant plant viral nucleic acid.

[0094] "Regulatory region" or "Regulatory sequence" as used herein in reference to a specific gene refers to the non-coding nucleotide sequences within that gene that are necessary or sufficient to provide for the regulated expression of the coding region of a gene. Thus the term regulatory region includes promoter sequences, regulatory protein binding sites, upstream activator sequences, and the like. Specific nucleotides within a regulatory region may serve multiple functions. For example, a specific nucleotide may be part of a promoter and participate in the binding of a transcriptional activator protein.

[0095] "Replication origin" as used herein, refers to the minimal terminal sequences in linear viruses that are necessary for viral replication.

[0096] "Replicon" as used herein, refers to an arrangement of RNA sequences generated by transcription of a transgene that is integrated into the host DNA that is capable of replication in the presence of a helper virus. A replicon may require sequences in addition to the replication origins for efficient replication and stability.

[0097] "Sample", as used herein, is used in its broadest sense. A biological sample suspected of containing a nucleic acid or fragments thereof may comprise a tissue, a cell, an extract from cells, chromosomes isolated from a cell (e.g., a spread of metaphase chromosomes), genomic DNA (in solution or bound to a solid support such as for Southern analysis), RNA (in solution or bound to a solid support such as for northern analysis), cDNA (in solution or bound to a solid support), and the like.

[0098] "Silent mutation" as used herein, refers to a mutation which has no apparent effect on the phenotype of the organism.

[0099] "Site-directed mutagenesis" as used herein, refers to the in-vitro induction of mutagenesis at a specific site in a given target nucleic acid molecule.

[0100] "Specific binding" or "specifically binding", as used herein, in reference to the interaction of an antibody and a protein or peptide, mean that the interaction is dependent upon the presence of a particular structure (i.e., the antigenic determinant or epitope) on the protein; in other words, the antibody is recognizing and binding to a specific protein structure rather than to proteins in general.

[0101] "Stringent conditions", as used herein, is the "stringency" which occurs within a range from about (T_m−5)° C. (i.e. 5 degrees below the melting temperature, T_m, of the probe) to about 20° to 25° C. below T_m. As will be understood by those of skill in the art, the stringency of hybridization may be altered in order to identify or detect identical or related polynucleotide sequences. Also as known in the art, numerous equivalent conditions may be employed to comprise either low or high stringency conditions. Factors such as the length and nature (DNA, RNA, base composition) of the sequence, nature of the target (DNA, RNA, base composition, presence in solution or immobilization, etc.), and the concentration of the salts and other components (e.g., the presence or absence of formamide, dextran sulfate and/or polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of either low or high stringency different from, but equivalent to, the above listed conditions.

[0102] "Subgenomic Promoter" as used herein, refers to a promoter of a subgenomic mRNA of a viral nucleic acid.

[0103] "Substantial Sequence Homology" as used herein, denotes nucleotide sequences that are substantially functionally equivalent to one another. Nucleotide differences between such sequences having substantial sequence homology will be de minimus in affecting function of the gene products or an RNA coded for by such sequence.

[0104] "Substitution", as used herein, refers to a change made in an amino acid of nucleotide sequence which results in the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

[0105] "Systemic Infection" as used herein denotes infection throughout a substantial part of an organism including mechanisms of spread other than mere direct cell inoculation but rather including transport from one infected cell to additional cells either nearby or distant.

[0106] "Transcription" as used herein, refers to the production of an RNA molecule by RNA polymerase as a complementary copy of a DNA sequence.

[0107] "Transcription termination region" as used herein, refers to the sequence that controls formation of the 3' end of the transcript. Self-cleaving ribozymes and polyadenylation sequences are examples of transcription termination sequences.

[0108] "Transformation" as used herein, describes a process by which exogenous DNA enters and changes a recipient cell. It may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed and may include, but is not limited to, viral infection, electroporation, lipofection, and particle bombardment. Such "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time.

[0109] "Transposon" as used herein refers to a nucleotide sequence such as a DNA or RNA sequence which is capable of transferring location or moving within a gene, a chromosome or a genome.

[0110] "Transgenic plant" as used herein refers to a plant which contains a foreign nucleotide sequence inserted into either its nuclear genome or organellar genome.

[0111] "Transcription" as used herein refers to the production of an RNA molecule by RNA polymerase as a complementary copy of a DNA sequence or subgenomic mRNA.

[0112] "Variants" of a gene product of interest, as used herein, refers to a sequence resulting when the gene product is altered by one or more amino acids. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have "nonconservative" changes, e.g., replacement of a glycine with a tryptophan. Variants may also include sequences with amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art.

[0113] "Vector" as used herein, refers to a self-replicating DNA or RNA molecule which transfers a DNA or RNA segment between cells.

[0114] "Virion" as used herein, refers to a particle composed of viral RNA and viral capsid protein.

[0115] "Virus" as used herein, refers to an infectious agent composed of a nucleic acid encapsidated in a protein. A virus may be a mono-, di-, tri- or multipartite virus.

THE INVENTION

[0116] Identification and Analysis of cDNAs

[0117] The invention is based on the discovery of 122 cDNAs, identified by the polynucleotide sequences SEQ ID NO: 1-122, that may be used to create transfected or

transgenic plants exhibiting a dwarf phenotype. Table 1 lists the source organism for all 122 cDNAs of the invention (as identified by its SEQ ID NO).

TABLE 1

SEQ ID NO.	Source	Sense or Antisense Configuration
1	*Nicotiana benthamiana*	A
2	*Nicotiana benthamiana*	A
3	*Arabidopsis thaliana*	S
4	*Arabidopsis thaliana*	S
5	*Arabidopsis thaliana*	S
6	*Arabidopsis thaliana*	S
7	*Arabidopsis thaliana*	S
8	*Arabidopsis thaliana*	A
9	*Arabidopsis thaliana*	A
10	*Arabidopsis thaliana*	A
11	*Arabidopsis thaliana*	A
12	*Arabidopsis thaliana*	A
13	*Arabidopsis thaliana*	A
14	*Arabidopsis thaliana*	A
15	*Arabidopsis thaliana*	A
16	*Arabidopsis thaliana*	A
17	*Arabidopsis thaliana*	A
18	*Arabidopsis thaliana*	A
19	*Arabidopsis thaliana*	A
20	*Arabidopsis thaliana*	A
21	*Arabidopsis thaliana*	A
22	*Arabidopsis thaliana*	A
23	*Arabidopsis thaliana*	A
24	*Arabidopsis thaliana*	A
25	*Arabidopsis thaliana*	A
26	*Arabidopsis thaliana*	A
27	*Arabidopsis thaliana*	A
28	*Arabidopsis thaliana*	A
29	*Arabidopsis thaliana*	A
30	*Arabidopsis thaliana*	A
31	*Arabidopsis thaliana*	A
32	*Arabidopsis thaliana*	A
33	*Arabidopsis thaliana*	A
34	*Arabidopsis thaliana*	A
35	*Arabidopsis thaliana*	A
36	*Arabidopsis thaliana*	A
37	*Arabidopsis thaliana*	A
38	*Arabidopsis thaliana*	A
39	*Arabidopsis thaliana*	A
40	*Arabidopsis thaliana*	A
41	*Arabidopsis thaliana*	A
42	*Arabidopsis thaliana*	A
43	*Arabidopsis thaliana*	A
44	*Arabidopsis thaliana*	A
45	*Arabidopsis thaliana*	A
46	*Arabidopsis thaliana*	A
47	*Arabidopsis thaliana*	A
48	*Arabidopsis thaliana*	A
49	*Arabidopsis thaliana*	A
50	*Arabidopsis thaliana*	A
51	*Arabidopsis thaliana*	A
52	*Arabidopsis thaliana*	A
53	*Arabidopsis thaliana*	A
54	*Arabidopsis thaliana*	A
55	*Arabidopsis thaliana*	A
56	*Arabidopsis thaliana*	A
57	*Arabidopsis thaliana*	A
58	*Arabidopsis thaliana*	A
59	*Arabidopsis thaliana*	A
60	*Arabidopsis thaliana*	A
61	*Arabidopsis thaliana*	A
62	*Arabidopsis thaliana*	A
63	*Arabidopsis thaliana*	A
64	*Arabidopsis thaliana*	A
65	*Arabidopsis thaliana*	A
66	*Arabidopsis thaliana*	A
67	*Arabidopsis thaliana*	A
68	*Arabidopsis thaliana*	A
69	*Arabidopsis thaliana*	A
70	*Arabidopsis thaliana*	A
71	*Arabidopsis thaliana*	A
72	*Arabidopsis thaliana*	A
73	*Arabidopsis thaliana*	A
74	*Arabidopsis thaliana*	A
75	*Arabidopsis thaliana*	A
76	*Arabidopsis thaliana*	A
77	*Arabidopsis thaliana*	A
78	*Arabidopsis thaliana*	A
79	*Arabidopsis thaliana*	A
80	*Arabidopsis thaliana*	A
81	*Arabidopsis thaliana*	A
82	*Arabidopsis thaliana*	A
83	*Arabidopsis thaliana*	A
84	*Arabidopsis thaliana*	A
85	*Arabidopsis thaliana*	A
86	*Arabidopsis thaliana*	A
87	*Arabidopsis thaliana*	A
88	*Arabidopsis thaliana*	A
89	*Arabidopsis thaliana*	A
90	*Arabidopsis thaliana*	A
91	*Arabidopsis thaliana*	A
92	*Arabidopsis thaliana*	A
93	*Arabidopsis thaliana*	A
94	*Arabidopsis thaliana*	A
95	*Arabidopsis thaliana*	A
96	*Arabidopsis thaliana*	A
97	*Arabidopsis thaliana*	S
98	*Arabidopsis thaliana*	A
99	*Arabidopsis thaliana*	n.d.
100	*Arabidopsis thaliana*	n.d.
101	*Arabidopsis thaliana*	n.d.
102	*Arabidopsis thaliana*	n.d.
103	*Arabidopsis thaliana*	n.d.
104	*Arabidopsis thaliana*	n.d.
105	*Arabidopsis thaliana*	n.d.
106	*Arabidopsis thaliana*	n.d.
107	*Arabidopsis thaliana*	n.d.
108	*Arabidopsis thaliana*	n.d.
109	*Arabidopsis thaliana*	n.d.
110	*Arabidopsis thaliana*	n.d.
111	*Arabidopsis thaliana*	n.d.
112	*Arabidopsis thaliana*	A
113	*Nicotiana benthamiana*	A
114	*Nicotiana benthamiana*	A
115	*Nicotiana benthamiana*	A
116	'Nicotiana benthamiana	S
117	*Oryza japonica*	S
118	*Oryza japonica*	S
119	*Oryza indica*	S
120	*Oryza indica*	S
121	*Papaver rhoeas*	S
122	*Oryza japonica*	S

[0118] The 122 cDNAs of the invention were identified by phenotypic screening and bioinformatic analysis of libraries of over 8000 cDNAs from Arabidopsis, Nicotiana, Oryza and Papaver constructed in the GENEWARE® vector. Table 1 lists whether the cDNA insert is in the sense (S) or antisense (A) configuration in the GENEWARE® vector used for the phenotypic screening. The use of the GENEWARE® vector in the field of genomics has been described in PCT WO 99/36516 published Jul. 22, 1999, which is herein incorporated by reference for all purposes. The general phenotypic screening method (described in greater detail below) involves constructing a GENEWARE® viral nucleic acid vector from each clone of

a normalized cDNA library of interest. Each GENEWARE® vector is then used to create an infectious viral unit which is applied to the individual plants of interest. Inoculation with GENEWARE® viral nucleic acid vectors results in a high rate of systemic infection of plants. The TMV based viral vector identified as PBSG1057 which has the ablility to transfect plants has been deposited under the Budapest Treaty at the AFCC and is designated ATCC #203981. Infected (and uninfected) plants are grown under identical conditions and an automated visual phenotypic analysis is conducted of each plant. The phenotypic data including descriptive of various parts of each plant is entered into a matrix-style database created using LIMS software. Once in the database, the phenotypic results are linked to the sequence data and bioinformatic analysis associated with each of the GENEWARE® vector (i.e. each cDNA in the library).

[0119] Out of over 8000 *Nicotiana benthamiana* plants infected by the GENEWARE®, 111 were discovered that exhibited a dwarf phenotype. Sequence analysis of these cDNAs (as described in greater detail below) yielded the identifying nucleic acid sequences SEQ. ID. NOs. 1-111. Bioinformatic analysis of these sequences using BLAST and other methods (described in greater detail below) yielded E.C. annotations for a large number of these sequences.

[0120] Further bioinformatic analysis of the 111 polynucleotide sequences identified an additional 34 cDNAs that may also function to cause dwarf phenotype in plants. Pfam analysis (described in greater detail below) of the 111 cDNAs identified SEQ ID NO:95 and 102 as members of the transketolase functional family, and the pfkb carbohydrate kinase family, respectively. Using this information, the 11 additional sequences (identified by SEQ ID NO: 112-122) were discovered in the LSBC GENEWARE® libraries that are either a member of the transketolase having the same metabolic activity as SEQ ID NO. 95, or a member pfkb carbohydrate kinase families having the same metabolic activity as SEQ ID NO. 102.

[0121] Following the identification of plants exhibiting the dwarf phenotype, biochemical analyses of tissue may be carried out in order to ascertain further details of the expressed cDNAs function. Methods including GC/MS analysis and Maldi-TOF analysis of the tissue have been carried out (described in greater detail below) and yield information on the profile of metabolites and proteins present in the infected plant's tissue. The results of these biochemical analyses are linked to the phenotype, sequence, and other bioinformatic data associated with each of the GENEWARE® vector. Using these biochemical analysis methods, and associated data processing techniques, the identification of at least one variation in the metabolome of an infected (versus an uninfected) plant may ascribe a function to the cDNA of interest.

[0122] According to the present invention, the dwarf phenotype may be created in a wide variety of plants or plant cell systems using the cDNAs identified by SEQ ID NO:1-122 and the various transformation methods described. In preferred embodiments, target plants and plant cells for engineering include, but are not limited to, monocotyledonous and dicotyledonous plants, including horticultural and ornamental plants (e.g., the grass and turfgrass species, and flowering plants such as petunia, rose, chrysanthemum), conifers and pine trees (e.g., pine, fir, spruce species, and including Abies sp., *Acer glabrum,* Pinus sp., Alnus sp., *Arbutus arizonica, Betula occidentalis,* Cedrus sp., Cryptomeriajaponica, Cupressus sp., Eucalyptus sp., *Ginkgo biloba,* Juniperus sp., *Libocedrus decurrens, Liriodendron tulipifera, Lithocarpus densiflora, Metasequoia glyptostroboides, P. ponderosa* var. *scopulorum,* Picea sp., Platanus sp., Populus sp., Pseudotsuga sp., *Purshia tridentata,* Quercus sp., Sequoia sp., *Taxus brevifolia,* Thuja sp., *Torreya californica, Tsuga heterophylla, Umbellularia californica*); plants used in phytoremediation (e.g., heavy metal accumulating plants), medicinal plants (e.g. *Solanaceae, Atropa belladonna, Duboisia myoporides, Hyoscymus niger, Scopolina atropoides, Solanum tuberosum, Eschscholtzia californica, Berberis stolonifera, Papaver somniferum*) and plants used for experimental purposes (e.g., *Arabidopsis thaliana*, Nicotiana sp.).

[0123] For a more complete listing of medicinal plants see Table 2. Another treatment of medicinal herbs can be found in, "1999 PDR for Herbal Medicines" 2nd edition, editors, Joerg Gruenwald et al.,, Medical Economics Company, Montvale, N.J., which is herein incorporated by reference for all purposes.

TABLE 2

Medicinal Plant	Medicinal Plant
Abies lasiocarpa	*Juglans major*
Abies excelsa	*Juniperus communis*
Abronia wootonii	*Juniperus monosperma*
Acacia arabica	*Juniperus sibirica*
Acacia catechu	*Kallstroemia grandiflora*
Acacia constricta	Kallstroemia spp.
Acacia greggii	*Kalmia angustifolia*
Acacia senegal	*Kalmia latifolia*
Acalypha californica	*Kalmia microphylla*
Acalypha lindheimeri	*Kalmia polifolia*
Achillea lanulosa	*Karwinskia humboldtiana*
Achillea millefolium	*Krameria grayi*
Achlys triphylla	*Krameria lanceolata*
Aconitum columbianum	*Krameria parvifolia*
Acorus calamus	*Lactuca serriola*
Actaea alba	*Lamium amplexicaule*
Actea rubra	*Larrea tridentata*
Adiantum capillus-veneris	*Ledum glandulosum*
Adiantum jordanii	*Ledum groenlandicum*
Adiantum pedatum	*Leonurus cardiaca*
Adoxa moschatellina	*Leonurus sibirica*
Aesculus californica	*Lepechinia calycina*
Aesculus glabra	*Lepidium montanum*
Aesculus hippocastanum	*Lespedeza violacea*
Aesculus pavia	*Leucophyllum frutescens*
Agastache urticifolia	*Levisticum ligusticum*
Agave chisoensis	*Lewisia rediviva*
Agave parryi	*Liatris punctata*
Agrimonia gryposepala	*Liatris squarrosa*
Agrimonia striata	*Ligusticum filicinum*
Agropyron repens	*Ligusticum grayi*
Alchemilla mollis	*Ligusticum porteri*
Alchemilla vulgaris	*Lilium grayi*
Aletris farinosa	*Lilium philadelphicum*
Alhagi camelorum	*Linaria canadensis*
Allium cernuum	*Linaria dalmatica*
Allium geyeri	*Linaria vulgaris*
Allium schoenoprasum	*Linnaea borealis*
Alnus incana	*Linum lewisii*
Aloe spp.	*Linum medium*
Aloe vera	*Linum usitatissimum*
Althea officinalis	*Liquidambar orientalis*
Amaranthus hybridus	*Liquidamber styraciflua*
Ambrosia ambrosioides	*Lithospermum arvense*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Ambrosia artemisiifolia	*Lithospermum multiflorum*
Ambrosia trifida	*Lithospermum ruderale*
Amelanchier alnifolia	*Lobelia cardinalis*
Amsinckia intermedia	*Lobelia cardinalis,*
Amsonia hirtella	*Lobelia cardinalis,*
Amygdalus persica	*Lobelia inflata*
Anaphalis margaritacea	*Lobelia kalmii*
Anemone deltoidea	*Lobelia siphilitica*
Anemone globosa	*Lomatium cous*
Anemone halleri	*Lomatium dissectum*
Anemone occidentalis	Lophocereus (Pachycereus)
Anemone patens	*Lycium fremontii*
Anemone patens,	*Lycium pallidum*
Anemone quinquefolia	*Lycopodium clavatum*
Anemone tuberosa	*Lycopus americanus*
Anemopsis californica	*Lycopus asper*
Anethum graveolens	*Lycopus uniflorus*
Angelica sp.	*Lycopus virginicus*
Angelica archangelica	*Lysichitum americanum*
Angelica arguta	*Lythrum salicaria*
Angelica dawsonii	*Macromeria viridiflora*
Angelica genuflexa	*Magnolia grandiflora*
Angelica grayi	*Mahonia aquifolia*
Angelica hendersonii	*Mahonia fremontii*
Angelica lineariloba	*Mahonia haematocarpa*
Angelica pinnata	*Mahonia nervosa*
Angelica venenosa	*Mahonia repens*
Antennaria howellii	*Mahonia trifoliata*
Antennaria rosea	*Mahonia wilcoxii*
Apocynum androsaemifolium	*Malus sylvestris*
Apocynum cannabinum	*Malva neglecta*
Apocynum medium	*Mammillaria arizonica*
Aquilegia caerulea	*Marah gilensis*
Aquilegia chrysantha	*Marrubium vulgare*
Aralia californica	*Matricaria chamomilla*
Aralia nudicaulis	*Matricaria matricarioides*
Aralia racemosa	*Medicago sativa*
Aralia spinosa	*Melampyrum lineare*
Arbutus menziesii	*Melilotus albus*
Arctium minus	*Menispermum canadense*
Arctostaphylos pungens	*Mentha arvensis*
Arctostaphylos uva-ursi	*Mentha pulegium*
Argemone corymbosa	*Mentha spicata*
Argemone mexicana	*Menyanthes trifoliata*
Argemone platyceras	*Mertensia ciliata*
Argemone polyanthemos	*Mimulus guttatus*
Arisaema atrorubens	*Mirabilis longiflora*
Arisaema dracontium	*Mirabilis multiflorum*
Arisaema stewardsonii	*Mitchella repens*
Arisaema triphyllum	*Monarda citriodora*
Aristolochia californica	*Monarda didyma*
Aristolochia serpentaria	*Monarda fistulosa*
Aristolochia watsonii	*Monarda media*
Arnica angustifolium	*Monarda menthaefolia*
Arnica cordifolia	*Monarda mollis*
Arnica latifolia	*Monarda pectinata*
Arnica mollis	*Monarda punctata*
Arnica montana	*Monardella villosa*
Artemisia douglasiana	*Moneses uniflora*
Artemisia filifolia	*Monotropa hypopitys*
Artemisia franserioides	*Monotropa uniflora*
Artemisia frigida,	*Mortonia scabrella*
Artemisia frigida	*Myrica californica*
Artemisia ludoviciana	*Myrica cerifera*
Artemisia tridentata	*Myristica fragrans*
Artemisia vulgaris	*Nelumbo lutea*
Asarum canadense	*Nepeta cataria*
Asarum caudatum	*Nicotiana attenuata*
Asclepias albicans	*Nicotiana glauca*
Asclepias asperula	*Nicotiana repanda*
Asclepias brachystephana	*Nicotiana tabacum*
Asclepias erosa	*Nicotiana trigonophylla*
Asclepias fascicularis	*Nuphar luteum*
Asclepias speciosa	*Nymphaea odorata*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Asclepias subulata	*Ocimum basilicum*
Asclepias syriaca	*Oenothera biennis*
Asclepias texana	*Oenothera hookeri*
Asclepias tuberosa	*Oplopanax horridum*
Asclepas viridis	*Opuntia erinacea*
Asclepias viridis	*Opuntia phaeacantha*
Asparagus officinale	*Orobanche fasciculata*
Aspidium filix-mas	*Orobanche ludoviciana*
Astragalus gummifer	*Orobanche uniflora*
Astragalus americanus	*Osmorhiza obtusa*
Astragalus membranaceus	*Osmorrhiza longistylis*
Atriplex canescens	*Osmorrhiza occidentalis*
Avena fatua	*Ourouparia gambir*
Avena sativa	*Oxalis cymosa*
Balsamorhiza sagittata	*Oxalis oregana*
Baptisia australis	*Oxalis metcalfei*
Baptisia leucantha	*Paeonia brownii*
Baptisia leucophaea	*Paeonia californica*
Baptisia sphaerocarpa	*Panax quinquefolium*
Baptisia tinctoria	*Panax trifolium*
Buddleya sp.	*Papaver rhoeas*
Berberis fendleri	*Papaver somniferum*
Berberis vulgaris	*Parthenium incanum*
Berberis -	*Parthenocissus inserta*
Besseya wyomingensis	*Parthenocissus quinquefolia*
Bidens frondosa	*Passiflora foetida*
Bidens pilosa	*Passiflora incarnata*
Bignonia capreolata	*Passiflora lutea*
Bouvardia ternifolia	*Passiflora sanguinea*
Brassica arvensis	*Paullinia cupana*
Brickellia amplexicaulis	*Pedicularis bracteosa*
Brickellia californica	*Pedicularis canadensis*
Brickellia grandiflora	*Pedicularis contorta*
Brugmansia sp.	*Pedicularis densiflora*
Bryonia alba	*Pedicularis grayii*
Bupleurum americanum	*Pedicularis groenlandica*
Bursera microphylla	*Pedicularis lanceolata*
Bursera odorata	*Pedicularis parryi*
Cacalia decomposita	*Pedicularis racemosa*
Caesalpinia gilliessii	*Peganum harmala*
Caesalpinia pulcherrima	*Peniocereus greggii*
Caffea arabica	*Penstemon cobaea*
Calendula officinalis	*Penstemon eatoni*
Callirhoe involucrata	*Penstemon lyallii*
Caltha biflora	*Perezia nana*
Caltha leptosepala	*Perezia wrightii*
Caltha palustris	*Perideridia gairdneri*
Calypso bulbosa	*Perilla frutescens*
Camassia quamash	*Petasites frigidus*
Camissonia (Oenothera)	*Petasites frigidus,*
Campsis radicans	*Petasites sagittatus*
Cannabis sativa	*Philadelphus lewisii*
Capsella bursa-pastoris	*Phoradendron flavescens*
Capsicum annuum	*Phoradendron juniperinum*
Capsicum frutescens	*Physalis crassifolia*
Cardamine cordifolia	*Physocarpus monogynus*
Carnegia gigantea	*Physostigma venenosum*
Cassia angustifolia	*Phytolacca americana*
Cassia covesii	*Picea engelmanni*
Cassia fasciculata	*Pinus contorta*
Cassia fistula	*Pinus edulis*
Cassia leptocarpa	*Pinus palustris*
Cassia marilandica	*Pinus ponderosa*
Cassia senna	*Pinus strobus*
Cassia wislizenii	*Pinus taeda*
Castanopsis chrysophylla	Piper sp
Castela emoryi	*Piper cubeba*
Castilleja sp.	*Plantago lanceolata*
Castilleja miniata	*Plantago major*
Caulophyllum thalictrioides	*Plantago patagonica*
Ceanothus americanus	*Plantago rugeli*
Ceanothus cuneatus	*Pluchea camphorata*
Ceanothus fendleri	*Podophyllum peltatum*
Ceanothus greggii	*Polygala alba*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Ceanothus herbaceum	*Polygala lutea*
Ceanothus spinosus	*Polygala obscura*
Ceanothus velutinus	*Polygala paucifolia*
Celastrus scandens	*Polygala senega*
Celtis occidentalis	*Polygonatum biflorum*
Centaurium venustum	*Polygonatum canaliculatum*
Cephaelis ipecacuanha	*Polygonum bistortioides*
Cephalanthus occidentalis	*Polymnia spp*
Cerastium arvense	*Polymnia canadensis*
Cercis occidentalis	*Polypodium glycyrriza*
Cercocarpus sp.	*Polystichum munitum*
Cetraria islandica	*Populus balsamifera*
Chamaelirium luteum	*Populus fremontii*
Chelidonium majus	*Populus tremulioides*
Chelone glabra	*Portulaca oleracea*
Chelone lyoni	*Potentilla diversifolia*
Chenopodium ambrosioides	*Potentilla fruticosa*
Chilopsis linearis	*Potentilla palustris*
Chimaphila umbellata	*Potentilla strigosa*
Chimaphila umbellata,	*Potentilla tridentata*
Chionanthus virginiana	*Proboscidea parviflora*
Chlorogalum pomeridianum	*Prosopis juliflora*
Chondrus crispus	*Prunella vulgaris*
Choisya arizonica	*Prunus americana*
Chrysanthemum leucanthemum	*Prunus avium*
Chrysanthemum parthenium	*Prunus laurocereus*
Cichorium intybus	*Prunus serotina*
Cicuta douglasii	*Prunus virginiana*
Cimicifuga arizonica	*Pseudotsuga menziesii*
Cimicifuga elata	*Psoralea esculenta*
Cimicifuga racemosa	*Ptelea pallida*
Cinchona succirubra	*Ptelea trifoliata*
Cinnamomum camphora	*Pulsatilla ludoviciana*
Cirsium undulatum	*Punica granatum*
Citrullus colocynthis	*Purshia tridentata*
Citrus sinensis	*Pyrola asarifolia*
Claviceps purpurea	*Pyrola minor*
Claytonia lanceolata	*Pyrola rotundifolia*
Clematis columbiana	*Pyrola secunda*
Clematis hirsutissima	*Prola virens*
Clematis ligusticifolia	*Quercus alba*
Clematis pseudoalpina	*Quercus gambelii*
Clematis viorna	*Quillaja saponaria*
Clematis virginiana	*Ratibida columnaris*
Cleome serrulata	*Rhamnus alnifolia*
Cocculus sp.	*Rhamnus betulifolia*
Cola nitida	*Rhamnus californica*
Colchicum autumnale	*Rhamnus frangula*
Collinsonia canadensis	*Rhamnus purshiana*
Commandra umbellata	*Rheum officinale*
Conium maculatum	*Rhus choriophylla*
Conopholis alpina	*Rhus glabra*
Conopholis americana	*Rhus microphylla*
Convallaria majus	Rhus (Toxicodendron)
Convolvulus arvensis	*Rhus trilobata*
Convolvulus scammonia	*Ribes aureum*
Conyza canadense	*Ricinus communis*
Copaiba langsdorffii	*Romneya coulteri*
Coptis groenlandica	*Rosa acicularis*
Coptis laciniata	*Rosa humilis*
Coptis occidentalis	*Rosa virginiana*
Corallorhiza maculata	*Rosa woodsii*
Corallorrhiza striata	*Rubus idaeus*
Cordia boissieri	*Rubus odoratus*
Cornus canadensis	*Rubus parviflorus*
Cornus florida	*Rudbeckia hirta*
Cornus stolonifera	*Rudbeckia laciniata*
Corydalis aureus	*Ruellia ciliosa*
Corydalis sempervirens	*Rumex acetosella*
Crataegus spp.	*Rumex crispus*
Crataegus columbiana	*Rumex hymenosepalus*
Crataegus douglasii	*Ruta graveolens*
Crataegus mollis	*Sabal texana*
Crataegus rivularis	*Sabatia angularis*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Crataegus succulenta	*Sabatia campestris*
Cucurbita foetidissima	*Sabatia stellaris*
Cupressus arizonica	*Sagittaria cuneata*
Cupressus macrocarpa	*Sagittaria latifolia*
Curcuma sp.	salix sp.
Cuscuta gronovi	*Salix discolor*
Cymopterus fendleri	*Salvia apiana*
Cynanchum nigrum	*Salvia azurea*
Cynara sp.	*Salvia clevelandii*
Cynoglossum officinale	*Salvia columbariae*
Cypripedium sp.	*Salvia greggii*
Cypripedium acaule	*Salvia henryi*
Cypripedium arietinum	*Salvia lemmonii*
Cypripedium calceolus	*Salvia leucophylla*
Cypripedium montanum	*Salvia mellifera*
Cypripedium parviflorum	*Salvia regla*
Cypripedium reginae	*Salvia reflexa*
Cytisus scoparius	*Salvia spathaceae*
Dalea formosa	*Sambucus canadensis*
Darlingtonia californica	*Sambucus mexicana*
Datura ferox	*Sambucus racemosa*
Datura metelioides	*Sanguinaria canadensis*
Datura wrightii	*Sanguisorba canadensis*
Daucus carota	*Sanicula marilandica*
Delphinium barbeyi	*Santalum album*
Delphinium elongatum	*Sanvitalia abertii*
Dendromecon rigida	*Sapindus saponaria*
Dicentra canadensis	*Saponaria officinalis*
Dicentra cucullaria	*Sarracenia psittacina*
Dicentra formosa	*Sarracenia purpurea*
Dicentra spectabilis	*Sarracenia rubra*
Digitalis purpurea	Sassafras IL
Dionaea muscipula	*Satureja douglasii*
Dioscorea villosa	*Saururus cernuus*
Dipsacus sylvestris	*Scopola carniolica*
Dipsacus fullonum	*Scrophularia californica*
Dodecathion pulchellum	*Scrophularia lanceolata*
Dracocephalum moldavica	*Scutellaria brittonii*
Dracocephalum parviflorum	*Scutellaria californica*
Drosera linearis	*Scutellaria drummondii*
Drosera rotundifolia	*Scutellaria epilobiifolia*
Dyssodia papposa	*Scuteliaria galericulata*
Ecballium elaterium	*Scutellaria incana*
Echevaria rusbyi	*Scutellaria integrifolia*
Echinacea angustifolia	*Scutellaria latiflora*
Echinacea pallida	*Scutellaria resinosa*
Echinacea purpurea	*Scutellaria serrata*
Echinacea tennessiensis	*Scutellaria tesselata*
Elettaria carmamomum	*Scutellaria wrightii*
Encelia farinosa	*Sedum rhodanthum*
Ephedra californica	*Sedum roseum*
Ephedra nevadensis	Selenicereus spp.
Ephedra torreyana	*Senecio aureus*
Ephedra trifurca	*Senecio cineraria*
Ephedra viridis	*Sequoia sempervirens*
Epifagus virginianum	*Serenoa repens*
Epigaea repens	*Shephardia argentea*
Epilobium angustifolium	*Shephardia canadensis*
Epilobium hirsutum	*Sida hederacea*
Epipactis gigantea	*Sidalcea neomexicana*
Epipactis helleborine	*Sidalcea malvaeflora*
Equisetum arvense	*Silphium laciniata*
Equisetum pratense	*Silphium perfoliatum*
Eremocarpus setigerus	*Silphium terebinthinaceum*
Eriodictyon angustifolia	*Silybum marianum*
Eriodictyon californica	*Simmondsia chinensis*
Eriodictyon crassifolium	*Smilacina racemosa*
Eriodictyon glutinosa	*Smilacina stellata*
Eriogonum leptophyllum	*Smilacina trifolia*
Eriogonum umbellata	Smilax spp.
Eriogonum wrightii	*Smilax californica*
Erodium cicutarium	*Smilax glauca*
Eryngium leavenworthii	*Smilax herbacea*
Eryngium lemmonii	*Smilax rotundifolia*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Eryngium yuccafolium	*Solanum carolinense*
Erysimum capitatum	*Solanum dulcamara*
Erythronium grandiflorum	*Solanum eleagnifolium*
Erythronium montanum	*Solanum nodiflorum*
Erythroxylon coca	*Solidago canadensis*
Eschscholtzia californica	*Sophora secundiflora*
Eschscholtzia mexicana	*Sorbus scopulina*
Eschscholtzia minutiflora	*Spartium junceum*
Eucalyptus sp.	*Sphaeralcea ambigua*
Euonymus occidentalis	*Sphaeralcea angustifolia*
Eupatorium coelestinum	*Sphaeralcea coccinea*
Eupatorium greggii	*Sphaeralcea fendleri*
Eupatorium herbaceum	*Sphaeralcea parviflora*
Eupatorium maculatum	*Sphenosciadium capitellatum*
Eupatorium perfoliatum	*Spigelia marilandica*
Eupatorium purpureum	*Spiraea alba*
Eupatorium rugosum	*Spiraea tomentosa*
Eustoma grandiflorum	*Stachys albens*
Eysenhardtia polystachya	*Stachys palustris*
Fallugia paradoxa	*Stachys rigida*
Ferula foetida	*Stellaria media*
Ferula galbaniflua	*Stenocereus thurberi*
Flourensia cernua	Sticta PH
Fouquieria splendens	*Stillingia sylvatica*
Fragaria glauca	*Streptopus amplexifolius*
Fragaria ovalis	*Strychnos nux-vomica*
Fragaria virginiana	*Swertia radiata*
Frankenia grandiflora	*Symphytum officinalis*
Frankenia palmeri	*Symplocarpus foetidus*
Fraxinus ornus	*Tanacetum huronense*
Fremontia californica	*Tanacetum parthenium*
Fritillaria atropurpurea	*Tanacetum vulgare*
Fritillaria pudica	Taraxacum sp.
Fucus vesiculosus	*Taxus brevifolia*
Fumaria officinalis	*Tecoma stans*
Gaillardia pinnatifida	*Teucrium laciniatum*
Galium aparine	*Thalictrum fendleri*
Galium borealis	*Thamnosma texana*
Garcinia hanburyi	*Thamnosma montana*
Garrya spp.	*Thelesperma gracile*
Garrya elliptica	*Tephrosia virginiana*
Garrya flavescens	*Thermopsis montana*
Garrya wrightii	*Thuja plicata*
Gaultheria procumbens	*Thymus vulgaris*
Gaultheria shallon	*Tillandsia recurvata*
Gaura lindheimeri	*Tillandsia usnioides*
Gaura parviflora	*Toluifera balsamum*
Gaylussacia brachycera	*Toluifera pereirae*
Gelsemium sempervirens	*Toxicodendron radicans*
Gentiana affinis	*Toxicodendron vernix*
Gentiana algida	*Tradescantia occidentalis*
Gentiana andrewsi	*Tragopogon dubius*
Gentiana calycosa	*Trautvettaria carolinensis*
Gentiana crinata	*Tribulus terrestrus*
Gentiana heterosepala	*Trichostema lanatum*
Gentiana parryi	*Trifolium pratense*
Gentiana saponaria	*Trillium erectum*
Gentiana simplex	*Trillium grandiflorum*
Gentiana thermalis	*Trillium ovatum*
Gentianella (Gentian)	*Trillium sessile*
Geranium maculatum	*Trillium undulatum*
Geranium richardsonii	*Trollius laxus*
Geranium viscosissimum	*Tsuga mertensiana*
Geum rivale	*Turnera diffusa*
Geum triflorum	*Umbellularia californica*
Gigartina mamillosa	*Urginea maritima*
Gillenia trifoliata	*Urtica dioica*
Glecoma hederacea	*Usnea barbata*
Glycyrriza glabra	*Usnea hirsutissima*
Glycyrrhiza lepidota	*Vaccinium corymbosum*
Gnaphallium sp.	*Vaccinium myrtillus*
Goodyera spp.	*Vaccinium ovatum*
Gossypium thurberi	*Vaccinium oxycoccos*
Grindelia aphanactis	*Vaccinium parvifolium*

TABLE 2-continued

Medicinal Plant	Medicinal Plant
Grindelia squarrosa	*Vaccinium scoparium*
Guaiacum angustifolium	*Vaccinium tenellum*
Guaiacum coulteri	*Vaccinium uliginosum*
Guaiacum sanctum	*Vaccinium vitis-idaea*
Gutierrezia sarothrae	*Valeriana acutiloba*
Habenaria blephariglottis	*Valeriana arizonica*
Habeneria fimbriata	*Valeriana edulus*
Habenaria (Plantanthera)	*Valeriana officinalis*
Hagenia abyssinica	*Valeriana occidentalis*
Hamamelis virginiana	*Valeriana sitchensis*
Haplopappus laricifolius	*Vancouveria hexandra*
Hedeoma hyssopifolium	*Veratrum californicum*
Hedeoma oblongifolia	*Veratrum viride*
Hedysarum alpinum	*Verbascum blattaria*
Helenium (Dugaldia)	*Verbascum thapsus*
Heliotropium convolvulaceum	*Verbena bipinnatifida*
Heracleum lanatum	*Verbena bracteata*
Heterotheca grandiflora	*Verbena canadensis*
Heterotheca psammophylla	*Verbena ciliata*
Heterotheca subaxillaris	*Verbena gooddingii*
Heuchera americanus	*Verbena hastata*
Heuchera micrantha	*Verbena macdougalii*
Heuchera parvifolia	*Verbena stricta*
Heuchera sanguinea	*Verbena wrightii*
Hibiscus moscheutos	*Verbesina encelioides*
Hibiscus oculiroseus	*Veronica americana*
Hierochloe odorata	*Veronica chamaedrys*
Holodiscus dumosus	Veronicastrum IM
Humulus americanus	*Viburnum acerifolium*
Humulus lupulus	*Viburnum americanum*
Hydrastis canadensis	*Viburnum cassinoides*
Hydrocotyle bonariensis	*Viburnum edule*
Hydrophyllum capitatum	*Viburnum ellipticum*
Hyocyamus niger	*Viburnum opulus*
Hypericum ascyron	*Viburnum prunifolium*
Hypericum aureum	*Viburnum rufidulum*
Hypericum formosum	*Vigueria dentata*
Hypericum perforatum	*Vinca major*
Hyptis emoryi	Viola sp
Hyssopus officinalis	*Viola canadensis*
Ilex vomitoria	*Viola pedata*
Impatiens biflora	*Viola tricolor*
Impatiens capensis	*Vitex agnus-castus*
Impatiens pallida	*Xanthium spinosum*
Indigofera sphaerocarpa	*Xanthium strumarium*
Inula helenium	*Xerophyllum tenax*
Ipomea arborescens	*Yucca baccata*
Ipomea jalapa	*Yucca baileyi*
Ipomea leptophylla	*Yucca elata*
Iris missouriensis	*Yucca schottii*
Iris prismatica	*Zanthoxylum fagaria*
Iris versicolor	*Zauschneria latifolia*
Jateorhiza palmata	*Zigadenus elegans*
Jatropha cardiophylla	*Zigadenus venenosus*
Jatropha dioica	Zingiber sp.
Jatropha macrorhiza	*Zizia aptera*
Jeffersonia diphylla	

[0124] The dwarf phenotype may be created using the cDNAs of the present invention in conjunction with a wide variety of plant virus expression vectors. The plant virus selected may depend on the plant system chosen and its known susceptibility to viral infection. Preferred embodiments of the plant virus expression vectors include, but are not limited to those in Table 3.

TABLE 3

Plant Viruses	Plant Viruses
Abelia latent tymovirus	Lucerne transient streak
Abutilon mosaic bigeminivirus	Lychnis ringspot hordeivirus
Ahlum waterborne carmovirus	Maclura mosaic macluravirus
Alfalfa 1 alphacryptovirus	Maize dwarf mosaic potyvirus
Alfalfa 2 betacryptovirus	Maize streak monogeminivirus
Alfalfa mosaic alfamovirus	Maracuja mosaic tobamovirus
Alsike clover vein mosaic virus	Marigold mottle potyvirus
Alstroemeria ilarvirus	Melandrium yellow fleck
Alstroemeria mosaic potyvirus	Melilotus mosaic potyvirus
Alstroemeria streak potyvirus	Melon Ourmia ourmiavirus
Amaranthus leaf mottle potyvirus	Melothria mottle potyvirus
Amaryllis alphacryptovirus	Milk vetch dwarf nanavirus
Amazon lily mosaic potyvirus	Mulberry latent carlavirus
Apple mosaic ilarvirus	Muskmelon vein necrosis carlavirus
Apple stem grooving capillovirus	Myrobalan latent ringspot nepovirus
Arabis mosaic nepovirus	Nandina mosaic potexvirus
Arracacha A nepovirus	Narcissus late season yellows
Arracacha A nepovirus	Narcissus latent macluravirus
Arracacha B nepovirus	Narcissus mosaic potexvirus
Arracacha Y potyvirus	Narcissus tip necrosis carmovirus
Artichoke Italian latent nepovirus	Narcissus tip necrosis carmovirus
Artichoke latent potyvirus	Narcissus yellow stripe potyvirus
Artichoke latent S carlavirus	Neckar River tombusvirus
Artichoke mottled crinkle	Nerine potyvirus
Artichoke vein banding nepovirus	Nicotiana velutina mosaic furovirus
Artichoke yellow ringspot	Oat blue dwarf marafivirus
Asparagus 1 potyvirus	Oat blue dwarf marafivirus
Asparagus 2 ilarvirus	Oat golden stripe furovirus
Asparagus 3 potexvirus	Odontoglossum ringspot
Aster chlorotic stunt carlavirus	Okra leaf-curl bigeminivirus
Asystasia gangetica mottle	Okra mosaic tymovirus
Aucuba ringspot badnavirus	Olive latent 1 sobemovirus
Barley stripe mosaic hordeivirus	Olive latent 2 ourmiavirus
Barley stripe mosaic hordeivirus	Onion mite-borne latent potexvirus
Barley yellow dwarf luteovirus	Onion yellow dwarf potyvirus
Barley yellow streak mosaic virus	Orchid fleck rhabdovirus
Bean calico mosaic bigeminivirus	Panicum mosaic sobemovirus
Bean common mosaic potyvirus	Papaya mosaic potexvirus
Bean distortion dwarf	Papaya ringspot potyvirus
Bean leaf roll luteovirus	Paprika mild mottle tobamovirus
Bean pod mottle comovirus	Parietaria mottle ilarvirus
Bean yellow mosaic potyvirus	Parsnip leafcurl virus
Beet curly top hybrigeminivirus	Parsnip mosaic potyvirus
Beet leaf curl rhabdovirus	Parsnip yellow fleck sequivirus
Beet mild yellowing luteovirus	Passiflora ringspot potyvirus
Beet mosaic potyvirus	Passionfruit woodiness potyvirus
Beet necrotic yellow vein furovirus	Patchouli mosaic potyvirus
Beet pseudo-yellows closterovirus	Pea early browning tobravirus
Beet soil-borne furovirus	Pea enation mosaic enamovirus
Beet western yellows leuteovirus	Pea mild mosaic comovirus
Beet yellows closterovirus	Pea mosaic potyvirus
Belladonna mottle tymovirus	Pea seed-borne mosaic potyvirus
Bidens mosaic potyvirus	Pea streak carlavirus
Black raspberry necrosis virus	Peach enation nepovirus
Blueberry leaf mottle nepovirus	Peach rosette mosaic nepovirus
Blueberry necrotic shock ilarvirus	Peanut chlorotic streak caulimovirus
Bramble yellow mosaic potyvirus	Peanut clump furovirus
Broad bean mottle bromovirus	Peanut mottle potyvirus
Broad bean necrosis furovirus	Peanut stunt cucumovirus
Broad bean stain comovirus	Peanut yellow spot tospovirus
Broad bean true mosaic comovirus	Pelargonium flower break
Broad bean wilt fabavirus	Pelargonium line pattern
Brome mosaic bromovirus	Pelargonium vein clearing
Burdock yellow mosaic potexvirus	Pelargonium zonate spot
Cacao necrosis nepovirus	Pepino mosaic potexvirus
Cacao swollen shoot badnavirus	Pepper Indian mottle potyvirus
Cacao yellow mosaic tymovirus	Pepper mild mosaic potyvirus
Cactus 2 carlavirus	Pepper mild mottle tobamovirus
Cactus X potexvirus	Pepper Moroccan tombusvirus
Canavalia maritima mosaic	Pepper mottle potyvirus
Caper latent carlavirus	Pepper ringspot tobravirus
Caraway latent nepovirus	Pepper severe mosaic potyvirus
Carnation rhabdovirus	Pepper Texas bigeminivirus
Carnation rhabdovirus	Pepper veinal mottle potyvirus

TABLE 3-continued

Plant Viruses	Plant Viruses
Carnation 1 alphacryptovirus	Petunia asteroid mosaic
Carnation 2 alphacryptovirus	Physalis mild chlorosis luteovirus
Carnation etched ring caulimovirus	Physalis mosaic tymovirus
Carnation Italian ringspot	Pineapple chlorotic leaf streak
Carnation latent carlavirus	Pineapple wilt-associated
Carnation mottle carmovirus	Pittosporum vein yellowing
Carnation mottle carmovirus	Plantain 6 carmovirus
Carnation necrotic fleck	Plantain 7 potyvirus
Carnation ringspot dianthovirus	Plantain X potexvirus
Carnation vein mottle potyvirus	Plum American line pattern ilarvirus
Carnation yellow stripe necrovirus	Plum pox potyvirus
Carrot mosaic potyvirus	Poinsettia mosaic tymovirus
Carrot mottle mimic umbravirus	Poplar mosaic carlavirus
Carrot mottle umbravirus	Poplar vein yellowing
Carrot yellow leaf closterovirus	Potato 14R tobamovirus
Cassava African mosaic	Potato A potyvirus
Cassava brown streak potyvirus	Potato Andean latent tymovirus
Cassava brown streak-associated	Potato Andean mottle comovirus
Cassava Caribbean mosaic	Potato aucuba mosaic potexvirus
Cassava Colombian symptomless	Potato black ringspot nepovirus
Cassava common mosaic	Potato leafroll luteovirus
Cassava green mottle nepovirus	Potato M carlavirus
Cassava Indian mosaic	Potato mop-top furovirus
Cassava Ivorian bacilliform	Potato mop-top furovirus
Cassava Ivorian bacilliform	Potato T trichovirus
Cassava X potexvirus	Potato U nepovirus
Cassia mild mosaic carlavirus	Potato V potyvirus
Cassia severe mosaic closterovirus	Potato X potexvirus
Celery latent potyvirus	Potato Y potyvirus
celery mosaic potyvirus	Potato yellow dwarf
Cherry leaf roll nepovirus	Primula mosaic potyvirus
Chickpea bushy dwarf potyvirus	Primula mottle potyvirus
Chickpea chlorotic dwarf	Prune dwarf ilarvirus
Chickpea distortion mosaic	Prunus necrotic ringspot ilarvirus
Chicory yellow mottle nepovirus	Radish mosaic comovirus
Chilli veinal mottle potyvirus	Raspberry ringspot nepovirus
Chino del tomat, bigeminivirus	Red clover mottle comovirus
Citrus leaf rugose ilarvirus	Red clover necrotic mosaic
Citrus ringspot virus	Red clover vein mosaic carlavirus
Clover mild mosaic virus	Rhynchosia mosaic bigeminivirus
Clover wound tumor phytoreovirus	Ribgrass mosaic tobamovirus
Clover wound tumor phytoreovirus	Rice hoja blanca tenuivirus
Clover yellow mosaic potexvirus	Rice stripe necrosis furovirus
Clover yellow vein potyvirus	Rice stripe tenuivirus
Colocasia bobone disease	Rose tobamovirus
Commelina X potexvirus	Rubus Chinese seed-borne
Cowpea chlorotic mottle	saguaro cactus carmovirus
Cowpea mild mottle carlavirus	Scrophularia mottle tymovirus
Cowpea mosaic comovirus	Shallot latent carlavirus
Cowpea mosaic comovirus	Shallot mite-borne latent potexvirus
Cowpea mottle carmovirus	Shallot yellow stripe potyvirus
Cowpea severe mosaic comovirus	Silene X potexvirus
Cowpea severe mosaic comovirus	Sint-Jan's onion latent carlavirus
Croton yellow vein mosaic	Sitke waterborne tombusvirus
Cucumber green mottle mosaic	Solanum apical leaf curling
Cucumber leaf spot carmovirus	Solanum nodiflorum mottle
Cucumber mosaic cucumovirus	Solanum nodiflorum mottle
Cucumber mosaic cucumovirus	Sonchus cytorhabdovirus
Cucumber necrosis tombusvirus	Sonchus yellow net
Cycas necrotic stunt nepovirus	Sorghum mosaic potyvirus
Cymbidium ringspot tombusvirus	Sowbane mosaic sobemovirus
Cynara nucleorhabdovirus	Soybean crinkle leaf bigeminivirus
Dahlia mosaic caulimovirus	Soybean dwarf luteovirus
Dandelion yellow mosaic	Soybean mild mosaic virus
sequivirus	Soybean mosaic potyvirus
Daphne Y potyvirus	Spinach latent ilarvirus
Dasheen bacilliform badnavirus	Spinach temperate alphacryptovirus
Dasheen mosaic potyvirus	Spring beauty latent bromovirus
Datura Colombian potyvirus	Statice Y potyvirus
Datura distortion mosaic potyvirus	Strawberry latent ringspot
Datura innoxia Hungarian mosaic	Subterranean clover red leaf
Datura mosaic potyvirus	Sugarcane mosaic potyvirus
Datura necrosis potyvirus	Sunflower ringspot ilarvirus
Datura shoestring potyvirus	Sunn-hemp mosaic tobamovirus

TABLE 3-continued

Plant Viruses	Plant Viruses
Datura yellow vein	Sweet clover latent
Desmodium mosaic potyvirus	Sweet clover necrotic mosaic
Dioscorea green banding mosaic	Sweet potato feathery mottle
Dioscorea latent potexvirus	Sweet potato latent potyvirus
Dogwood mosaic nepovirus	Sweet potato mild mottle
Dulcamara mottle tymovirus	Sweet potato ringspot nepovirus
Eggplant green mosaic potyvirus	Sweet potato sunken vein
Eggplant mild mottle carlavirus	Tamarillo mosaic potyvirus
Eggplant mottled crinkle	Tamus latent potexvirus
Eggplant mottled dwarf	Telfairia mosaic potyvirus
Eggplant severe mottle potyvirus	Tobacco etch potyvirus
Elderberry carlavirus	Tobacco leaf curl bigeminivirus
Elderberry latent carmovirus	Tobacco mild green mosaic
Elm mottle ilarvirus	Tobacco mosaic satellivirus
Epirus cherry ourmiavirus	Tobacco mosaic tobamovirus
Erysimum latent tymovirus	Tobacco mottle umbravirus
Eucharis mottle nepovirus	Tobacco necrosis necrovirus
Euphorbia mosaic bigeminivirus	Tobacco necrosis satellivirus
Foxtail mosaic potexvirus	Tobacco necrotic dwarf luteovirus
Foxtail mosaic potexvirus	Tobacco rattle tobravirus
Foxtail mosaic potexvirus	Tobacco ringspot nepovirus
Frangipani mosaic tobamovirus	Tobacco streak ilarvirus
Furcraea necrotic streak	Tobacco stunt varicosavirus
Galinsoga mosaic carmovirus	Tobacco vein mottling potyvirus
Garlic common latent carlavirus	Tobacco vein-distorting luteovirus
Glycine mottle carmovirus	Tobacco wilt potyvirus
Grapevine A trichovirus	Tobacco yellow dwarf
Grapevine ajinashika disease	Tobacco yellow net luteovirus
Grapevine Algerian latent	Tobacco yellow vein umbravirus
Grapevine B trichovirus	Tobacco yellow vein assistor
Grapevine Bulgarian latent	Tomato aspermy cucumovirus
Grapevine chrome mosaic	Tomato Australian leafcurl
Grapevine chrome mosaic	Tomato black ring nepovirus
Grapevine corky bark-associated	Tomato black ring nepovirus
Grapevine fanleaf nepovirus	Tomato bushy stunt tombusvirus
Grapevine fleck virus	Tomato golden mosaic
Grapevine leafroll-associated	Tomato mild mottle potyvirus
Grapevine line pattern ilarvirus	Tomato mosaic tobamovirus
Grapevine stem pitting associated	Tomato mottle bigeminivirus
Grapevine stunt virus	Tomato Peru potyvirus
Groundnut chlorotic spot	Tomato ringspot nepovirus
Groundnut rosette umbravirus	Tomato spotted wilt tospovirus
Guar top necrosis virus	Tomato top necrosis nepovirus
Habenaria mosaic potyvirus	Tomato yellow leaf curl
Helenium S carlavirus	Tropaeolum 1 potyvirus
Henbane mosaic potyvirus	Tropaeolum 2 potyvirus
Heracleum latent trichovirus	Tulare apple mosaic ilarvirus
Hibiscus latent ringspot nepovirus	Tulip chlorotic blotch potyvirus
Hippeastrum mosaic potyvirus	Tulip halo necrosis virus
Honeysuckle latent carlavirus	Tulip X potexvirus
Hop American latent carlavirus	Turnip crinkle carmovirus
Hop latent carlavirus	Turnip mosaic potyvirus
Humulus japonicus ilarvirus	Turnip rosette sobemovirus
Hydrangea mosaic ilarvirus	Turnip yellow mosaic tymovirus
Impatiens latent potexvirus	Ullucus mild mottle tobamovirus
Impatiens necrotic spot tospovirus	Ullucus mosaic potyvirus
Iris fulva mosaic potyvirus	Vallota mosaic potyvirus
Ivy vein clearing cytorhabdovirus	Vanilla necrosis potyvirus
Johnsongrass mosaic potyvirus	Viola mottle potexvirus
Kalanchoe isometric virus	Viola mottle potexvirus
Konjak mosaic potyvirus	Watercress yellow spot virus
Kyuri green mottle mosaic	Watermelon mosaic 1 potyvirus
Lamium mild mottle fabavirus	Watermelon mosaic 2 potyvirus
Lato River tombusvirus	Weddel waterborne carmovirus
Leek yellow stripe potyvirus	Welsh onion yellow stripe
Lettuce big-vein varicosavirus	Wheat soil-borne mosaic furovirus
Lettuce infectious yellows	Wheat streak mosaic rymovirus
Lettuce mosaic potyvirus	White clover mosaic potexvirus
Lettuce necrotic yellows	Wild cucumber mosaic tymovirus
Lettuce speckles mottle umbravirus	Wild potato mosaic potyvirus
Lilac chlorotic leafspot capillovirus	Wild potato mosaic potyvirus
Lilac ring mottle ilarvirus	Wineberry latent virus
Lily X potexvirus	Wisteria vein mosaic potyvirus
Lisianthus necrosis necrovirus	Yam mosaic potyvirus

TABLE 3-continued

Plant Viruses	Plant Viruses
Lucerne Australian latent nepovirus	Zygocactus Montana X potexvirus
Lucerne Australian symptomless	
Lucerne enation nucleorhabdovirus	

[0125] A further listing of plants and plant viruses that may used with the methods of the invention is shown in Table 4. Additional examples of virus infections of plant species can be found at: http://image.fs.uidaho.edu/vide/. Additional virus accessions can be retrieved at: http://www.atcc.org.

TABLE 4

Plant or Virus Name	Plant or Virus Name
Cryptomeria japonica	Tulip band-breaking
Eucalyptus grandis	potyvirus
Eucalyptus nitens	Tulip breaking potyvirus
Eucalyptus urophylla	Tulip chlorotic blotch
Picea abies	potyvirus
Picea glauca	Tulip halo necrosis (?) virus
Pinus albicaulis	Tulip X potexvirus
Pinus aristata	*Linum usitatissimum*
Pinus armandii	Synonyms:
Pinus attenuata	*Linum crepitans*; *Linum*
Pinus ayacahuite	*humile*; *Linum usitatissimum* ssp.
Pinus balfouriana	*transitorium*; *Linum usitatissimum*
Pinus brutia	var. *humile*
Pinus bungeana	Common names:
Pinus canariensis	Flax; Linseed; Lino
Pinus cembroides	Susceptible to:
Pinus contorta	Alfalfa mosaic alfamovirus
Pinus culminicola	Beet curly top
Pinus durangensis	hybrigeminivirus
Pinus echinata	Beet pseudo-yellows (?)
Pinus edulis	closterovirus
Pinus elliottii	Oat blue dwarf marafivirus
Pinus engelmannii	Tobacco rattle tobravirus
Pinus flexilis	Hibiscus
Pinus gerardiana	Susceptible to:
Pinus griffithii	Abutilon mosaic
Pinus halepensis	bigeminivirus
Pinus hartwegii	Cotton leaf crumple
Pinus jefferyi	bigeminivirus
Pinus koraiensis	Hibiscus yellow mosaic (?)
Pinus lambertiana	tobamovirus
Pinus lumholtzii	*Hibiscus cannabinus*
Pinus massoniana	Common names:
Pinus monticola	Deccan-hemp; Indian-hemp;
Pinus mugo	Kenaf
Pinus palustris	Susceptible to:
Pinus pinaster	Cotton anthocyanosis (?)
Pinus pinceana	luteovirus
Pinus ponderosa	Cotton leaf crumple
Pinus pungens	bigeminivirus
Pinus radiata	Cotton leaf curl
Pinus resinosa	bigeminivirus
Pinus roxburghii	Hibiscus chlorotic ringspot
Pinus sabiniana	carmovirus
Pinus serotina	Hibiscus latent ringspot
Pinus strobus	nepovirus
Pinus sylvestris	Kenaf vein-clearing (?)
Pinus tabulaeformis	rhabdovirus
Pinus taeda	Malva vein clearing
Pinus thunbergii	potyvirus
Pinus torreyana	Okra mosaic tymovirus
Pinus virginiana	*Ficus carica*
Pinus wangii	Common names:
Pinus yunnanensis	Fig; Higo

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Populus deltoides	Susceptible to:
Populus tremuloides	Fig (?) potyvirus
Cryptomeria japonica	Fig S carlavirus
Eucalyptus grandis	*Morus alba*
Eucalyptus nitens	Synonyms:
Eucalyptus urophylla	*Morus alba* f. *tatarica*;
Picea abies	*Morus alba* var.
Picea glauca	*constantinopolitana*; *Morus alba*
Pinus albicaulis	var. *multicaulis*; *Morus indica*;
Pinus aristata	*Morus multicaulis*
Pinus armandii	Common names:
Pinus attenuata	White mulberry; Mora
Pinus ayacahuite	Susceptible to:
Pinus balfouriana	Citrus enation- woody gall
Pinus brutia	(?) luteovirus
Pinus bungeana	Mulberry latent carlavirus
Pinus canariensis	Mulberry ringspot
Pinus cembroides	nepovirus
Pinus contorta	*Mirabilis jalapa*
Pinus culminicola	Common names:
Pinus durangensis	Common four-o'clock
Pinus echinata	Susceptible to:
Pinus edulis	Mirabilis mosaic
Pinus elliottii	caulimovirus
Pinus engelmannii	*Fraxinus excelsior*
Pinus flexilis	Synonyms:
Pinus gerardiana	*Fraxinus excelsior* var.
Pinus griffithii	*pendula*
Pinus halepensis	Common names:
Pinus hartwegii	European ash
Pinus jefferyi	Susceptible to:
Pinus koraiensis	Arabis mosaic nepovirus
Pinus lambertiana	*Jasminum officinale*
Pinus lumholtzii	Common names:
Pinus massoniana	Poet's jasmine; Common
Pinus monticola	jasmine; Jessamine
Pinus mugo	Susceptible to:
Pinus palustris	Arabis mosaic nepovirus
Pinus pinaster	*Ligustrum vulgare*
Pinus pinceana	Synonyms:
Pinus ponderosa	*Ligustrum insulare*;
Pinus pungens	*Ligustrum insulense*
Pinus radiata	Common names:
Pinus resinosa	Common privet
Pinus roxburghii	Susceptible to:
Pinus sabiniana	Arabis mosaic nepovirus
Pinus serotina	Petunia asteroid mosaic
Pinus strobus	tombusvirus
Pinus sylvestris	*Olea europaea*
Pinus tabulaeformis	Common names:
Pinus taeda	Olive; Aceituna
Pinus thunbergii	Susceptible to:
Pinus torreyana	Cherry leaf roll nepovirus
Pinus virginiana	Olive latent ringspot
Pinus wangii	nepovirus
Pinus yunnanensis	Olive latent 1 (?)
Populus deltoides	sobemovirus
Populus tremuloides	Olive latent 2 (?)
Populus trichocarpa	ourmavirus
Pseudotsuga menziesii	*Oenothera biennis*
Taxus brevifolia	Synonyms:
Ulmus parvifolia	*Oenothera biennis* ssp.
Chamaecyparis lawsoniana	*sulfurea*; *Oenothera chicagoensis*;
Common names:	*Oenothera muricata*; *Oenothera*
Port Orford-cedar; Ginger-	*suaveolens*; *Onagra biennis*
pine; Oregon-cedar; Lawson's	Common names:
cypress	Common evening-primrose;
Susceptible to:	German rampion
Arabis mosaic nepovirus	Insusceptible to:
Eucalyptus cloeziana	Carnation vein mottle
Common names:	potyvirus
Cloeziana gum; Gympie	Cymbidium
messmate	Susceptible to:
Populus balsamifera	Cymbidium mosaic

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Susceptible to:	potexvirus
Poplar mosaic carlavirus	Cymbidium ringspot
Poplar vein yellowing (?)	tombusvirus
nucleorhabdovirus	*Cymbidium alexanderi*
Populus candicans	Susceptible to:
Synonyms:	Odontoglossum ringspot
Populus balsamifera ssp.	tobamovirus
balsamifera; *Populus tacamahacca*	*Odontoglossum grande*
Common names:	Synonyms:
Balsam poplar; Tacamahac	*Rossioglossum grande*
poplar; Balm of Gilead	Susceptible to:
Susceptible to:	Odontoglossum ringspot
Poplar mosaic carlavirus	tobamovirus
Populus deltoides subspecies	*Cocos nucifera*
angulata, *monilifera*,	Common names:
missouriensis	Coconut; Coconut palm;
Susceptible to:	Copra; Khopra; Nariyal; Coco
Poplar mosaic carlavirus	Susceptible to:
Ulmus americana	Coconut foliar decay
Common names:	nanavirus
American elm	*Papaver nudicaule*
Susceptible to:	Synonyms:
Cherry leaf roll nepovirus	*Papaver miyabeanum*
Ulmus glabra	Common names:
Synonyms:	Iceland poppy; Arctic poppy
Ulmus montana; *Ulmus*	Susceptible to:
scabra	Beet curly top
Common names:	hybrigeminivirus
Scotch elm; Wych elm	Tobacco mosaic
Susceptible to:	tobamovirus
Elm mottle ilarvirus	Tomato spotted wilt
Ulmus minor	tospovirus
Synonyms:	Turnip mosaic potyvirus
Ulmus campestris; *Ulmus*	*Papaver somniferum*
carpinifolia; *Ulmus carpinifolia*	Common names:
var. *suberosa*; *Ulmus foliacea*	Opium poppy
Ulmus foliacea var. *suberosa;*	Susceptible to:
Ulmus glabra var.	Bean yellow mosaic
suberosa; *Ulmus nitens;*	potyvirus
Ulmus suberosa	*Papaver rhoeas*
Susceptible to:	Common names:
Elm mottle ilarvirus	Corn poppy; Shirley poppy;
Subject: turf	Field poppy
Agropyron cristatum	Susceptible to:
Festuca arizonica	Beet western yellows
Agropyron cristatum x	clostreovirus
desertorum	*Sesamum indicum*
Festuca arundinacea	Synonyms:
Agropyron dasystachyum	*Sesamum orientale*
Festuca duriuscula	Common names:
Agropyron desertorum	Sesame; Benne seed
Festuca eliator	Susceptible to:
Agropyron elongatum	Abelia latent tymovirus
Festuca eliator	Apple stem pitting virus
arundinacea	Arracacha A nepovirus
Agropyron inerme	Asparagus 3 potexvirus
Festuca idahoensis	Asystasia gangetica mottle (?)
Agropyron intermedium	potyvirus
Festuca longifolia	Blackgram mottle (?)
Agropyron riparium	carmovirus
Festuca megalura	Cassia yellow spot
Agropyron sibericum	potyvirus
Festuca ovina	Cherry leaf roll nepovirus
Agropyron smithii	Citrus ringspot virus
Festuca rubra	Lisianthus necrosis (?)
Agropyron spicatum	necrovirus
Festuca rubra var.	Malva veinal necrosis (?)
commutata	potexvirus
Agropyron spicatum x	Melothria mottle (?)
repens	potyvirus
Festuca rubra var. *rubra*	Mulberry latent carlavirus
Agropyron trachycaulum	Mulberry ringspot
Hordeum brachyantherum	nepovirus
Agropyron trichophorum	Okra mosaic tymovirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Koeleria cristata	Patchouli mottle (?)
Agrostis alba	potyvirus
Lolium multiflorum	Pea stem necrosis virus
Agrostis palustris	Peach enation (?) nepovirus
Lolium perenne	Peanut green mosaic
Agrostis tenuis	potyvirus
Oryzopsis hymenoides	Peanut mottle potyvirus
Alopecurus arundinaceus	Peanut stunt cucumovirus
Phalaris arundinacea	Satsuma dwarf (?)
Alopecurus pratensis	nepovirus
Phleum alpinum	Soybean mild mosaic virus
Arcatagrostis latifolia	Sweet potato yellow dwarf
Phleum pratense	(?) ipomovirus
Beckmannia syzigachne	Tobacco ringspot nepovirus
Phragmites australis	Watermelon mosaic 2
Bromus biebersteinii	potyvirus
Poa alpina	*Phytolacca americana*
Bromus carinatus	Synonyms:
Poa ampla	*Phytolacca decandra*
Bromus catharticus	Common names:
Poa bulbosa	Pokeweed; Poke;
Bromus inermis	Pigeonberry
Poa canbyi	Susceptible to:
Bromus marginatus	Alfalfa mosaic alfamovirus
Poa compressa	Bean yellow mosaic
Bromus mollis	potyvirus
Poa glauca	Beet curly top
Dactylis glomerata	hybrigeminivirus
Poa palustris	Beet mosaic potyvirus
Deschampsia caespitosa	Carnation mottle
Poa pratensis	carmovirus
Viruses for Graminae:	Carnation ringspot
Maize streak monogeminivirus	dianthovirus
Wheat streak mosaic rymovirus	Cucumber mosaic
Barley yellow dwarf luteovirus	cucumovirus
Barley stripe mosaic hordeivirus	Cymbidium ringspot
Sugarcane mosaic potyvirus	tombusvirus
Beet western yellows luteovirus	Pepper veinal mottle
Maize dwarf mosaic potyvirus	potyvirus
Foxtail mosaic potexvirus	Pokeweed mosaic potyvirus
Johnsongrass mosaic potyvirus	Red clover necrotic mosaic
Panicum mosaic (?) sobemovirus	dianthovirus
Rice stripe tenuivirus	Tobacco rattle tobravirus
Rice hoja blanca tenuivirus	Tobacco ringspot nepovirus
Wheat yellow leaf closterovirus	Tomato black ring
Brome mosaic bromovirus	nepovirus
Ribgrass mosaic tobamovirus	Turnip mosaic potyvirus
Wheat soil-borne mosaic furovirus	*Plantago major*
Deschampsia caespitosa (L.)	Common names:
Beauv. ssp. Beringensis	Common plantain;
Poa sandbergii	Broadleaf plantain; Great plantain
Elymus angustus	Susceptible to:
Poa trivialis	Carnation vein mottle
Elymus canadensis	potyvirus
Puccinellia distans	Cherry rasp leaf nepovirus
Elymus cinereus	Plantago 4 (?) caulimovirus
Secale cereale	Plantago mottle tymovirus
Elymus dahuricus	Ribgrass mosaic
Sitanion hystrix	tobamovirus
Elymus glaucus	*Phlox drummondii*
Stipa comata	Common names:
Elymus junceus	Drummond phlox; Annual
Stipa viridula	phlox
Elymus triticoides	Susceptible to:
Triticum aestivum, spp.	Apple mosaic ilarvirus
WARM SEASON GRASSES	Arabis mosaic nepovirus
Andropogon geradii	Beet curly top
Distichlis stricta	hybrigeminivirus
Andropogon hallii	Beet western yellows
Panicum virgatum	luteovirus
Bouteloua curtipendula	Carnation ringspot
Schizachyrium scoparium	dianthovirus
Bouteloua gracillis	Cherry leaf roll nepovirus
Sorghastrum nutans	Cymbidium ringspot

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Buchloe dactyloides	tombusvirus
Sporobolus airoides	Dogwood mosaic (?)
Calamovilfa longifolia	nepovirus
Sporobolus crypatandrus	Elm mottle ilarvirus
Cynodon dactylon	Melon Ourmia ourmiavirus
LEGUMES	Okra mosaic tymovirus
Astragalus cicer	Poplar mosaic carlavirus
Onobrychis viciaefolia	Prune dwarf ilarvirus
Coronilla varia	Ribgrass mosaic
Trifolium hybridum	tobamovirus
Hedysarum boreale	Spinach latent ilarvirus
Trifolium pratense	Strawberry latent ringspot
Lotus corniculatus	(?) nepovirus
Trifolium repens	Sweet potato mild mottle
Lupinus spp.	ipomovirus
Trifolium repens L.	Tobacco ringspot nepovirus
Medicago sativa	Tobacco streak ilarvirus
Vicia villosa	Tomato spotted wilt
Melilotus officinalis	tospovirus
Tritolium ambigium	*Polypodium vulgare*
Astragalus glycyphyllos	Susceptible to:
Common names:	Fern (?) potyvirus
Liquorice milk-vetch	rimula malacoides
Susceptible to:	Susceptible to:
Alfalfa mosaic alfamovirus	Carnation mottle
Astragalus sinicus	carmovirus
Susceptible to:	Hydrangea ringspot
Bean leaf roll luteovirus	potexvirus
Milk vetch dwarf nanavirus	Primula mottle (?) potyvirus
Soybean dwarf luteovirus	Sweet potato mild mottle
Subterranean clover red leaf	ipomovirus
luteovirus	Viola mottle potexvirus
Subterranean clover stunt	Pteris 'Childsii'
nanavirus	Susceptible to:
Watermelon mosaic 2	Harts tongue fern (?)
potyvirus	tobravirus
Coronilla varia	*Ranunculus repens*
Synonyms:	Common names:
Securigera varia	Creeping buttercup
Common names:	Susceptible to:
Crown-vetch; Trailing	Arabis mosaic nepovirus
crown-vetch	Ranunculus repens
Susceptible to:	symptomless (?) rhabdovirus
Peanut stunt cucumovirus	*Malus domestica*
Trifolium hybridum	Synonyms:
Common names:	*Malus malus*; *Pyrus malus*
Alsike clover; Swedish	Common names:
clover; Trefle-hybride; Trefle-	Apple; Common apple
batard; Schwedenklee;	Susceptible to:
Bastardklee; Trevo-hibrido;	Apple mosaic ilarvirus
Trebol-hibrido	Insusceptible to:
Susceptible to:	Plum pox potyvirus
Alfalfa mosaic alfamovirus	*Malus platycarpa*
Alsike clover vein mosaic	Susceptible to:
virus	Apple chlorotic leaf spot
Bean leaf roll luteovirus	trichovirus
Bean yellow mosaic	Apple stem pitting virus
potyvirus	*Malus sylvestris*
Beet curly top	Common names:
hybrigeminivirus	Crab apple; Wild apple
Beet yellows closterovirus	Susceptible to:
Broad bean mottle	Apple chlorotic leaf spot
bromovirus	trichovirus
Broad bean stain comovirus	Apple stem grooving
Clover mild mosaic virus	capillovirus
Clover yellow mosaic	Apple stem pitting virus
potexvirus	Cherry rasp leaf nepovirus
Clover yellow vein	Horseradish latent
potyvirus	caulimovirus
Cucumber mosaic	Tomato ringspot nepovirus
cucumovirus	Tulare apple mosaic
Muskmelon vein necrosis	ilarvirus
carlavirus	*Prunus avium*
Pea early browning	Synonyms:

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
tobravirus	*Cerasus avium* var.
Pea enation mosaic	*aspleniifolia*; *Prunus avium* var.
enamovirus	*aspleniifolia*; *Prunus cerasus* var.
Pea streak carlavirus	*avium*
Peanut stunt cucumovirus	Common names:
Red clover mottle	Mazzard cherry; Sweet
comovirus	cherry
Red clover vein mosaic	Susceptible to:
carlavirus	Arabis mosaic nepovirus
Soybean dwarf luteovirus	Cherry leaf roll nepovirus
Subterranean clover red leaf	Cherry mottle leaf (?)
luteovirus	trichovirus
Tomato ringspot nepovirus	Cherry rasp leaf nepovirus
Turnip mosaic potyvirus	Epirus cherry ourmiavirus
White clover mosaic	Myrobalan latent ringspot
potexvirus	nepovirus
Lotus corniculatus	Petunia asteroid mosaic
Synonyms:	tombusvirus
Lotus corniculatus ssp.	*Prunus domestica*
major; *Lotus corniculatus* var.	Common names:
major; *Lotus major*	Plum
Common names:	Susceptible to:
Bird's-foot trefoil	Apple chlorotic leaf spot
Susceptible to:	trichovirus
Cucumber mosaic	Arabis mosaic nepovirus
cucumovirus	Citrus enation-woody gall
Lupinus albus	(?) luteovirus
Common names:	Petunia asteroid mosaic
White lupine; Egyptian	tombusvirus
lupine	Plum American line pattern
Susceptible to:	ilarvirus
Alfalfa mosaic alfamovirus	Plum pox potyvirus
Amaranthus leaf mottle	Prune dwarf ilarvirus
potyvirus	Sowbane mosaic
Bean common mosaic	sobemovirus
potyvirus	Strawberry latent ringspot
Bean yellow mosaic	(?) nepovirus
potyvirus	*Prunus persica*
Beet western yellows	Synonyms:
luteovirus	*Amygdalus persica*;
Bidens mosaic potyvirus	*Amygdalus persica* var.
Broad bean mottle	*camelliiflora*; *Amygdalus persica*
bromovirus	var. *densa*; *Persica vulgaris*;
Broad bean true mosaic	*Prunus persica* var. *camelliiflora*;
comovirus	*Prunus persica* var. *densa*
Carnation yellow stripe (?)	Common names:
necrovirus	Peach; Melocotonero;
Cassia mild mosaic (?)	Abridor; Durazno
carlavirus	Susceptible to:
Chicory yellow mottle	Apple chlorotic leaf spot
nepovirus	trichovirus
Cowpea chlorotic mottle	Arabis mosaic nepovirus
bromovirus	Cherry leaf roll nepovirus
Cucumber mosaic	Cherry mottle leaf (?)
cucumovirus	trichovirus
Dogwood mosaic (?)	Cherry rasp leaf nepovirus
nepovirus	Myrobalan latent ringspot
Epirus cherry ourmiavirus	nepovirus
Glycine mottle (?)	Peach enation (?) nepovirus
carmovirus	Peach rosette mosaic
Lucerne Australian latent	nepovirus
nepovirus	Peach yellow leaf (?)
Lucerne transient streak	closterovirus
sobemovirus	Plum American line pattern
Pea enation mosaic	ilarvirus
enamovirus	Plum pox potyvirus
Pea streak carlavirus	Prune dwarf ilarvirus
Peanut mottle potyvirus	Prunus necrotic ringspot
Peanut stunt cucumovirus	ilarvirus
Pepper Moroccan	Strawberry latent ringspot
tombusvirus	(?) nepovirus
Plum pox potyvirus	Tomato ringspot nepovirus
Prunus necrotic ringspot	*Pyrus communis*
ilarvirus	Synonyms:

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Ribgrass mosaic	*Pyrus asiae-mediae*; *Pyrus*
tobamovirus	*balansae*; *Pyrus bourgaeana*;
Soybean dwarf luteovirus	*Pyrus domestica*; *Pyrus elata*;
Soybean mild mosaic virus	*Pyrus medvedevii*
Soybean mosaic potyvirus	Common names:
Subterranean clover red leaf	Pear; Pera
luteovirus	Susceptible to:
Turnip mosaic potyvirus	Apple chlorotic leaf spot
Watermelon mosaic 2	trichovirus
potyvirus	Apple stem pitting virus
Wisteria vein mosaic	Rosa
potyvirus	Susceptible to:
Medicago sativa	Apple mosaic ilarvirus
Synonyms:	Arabis mosaic nepovirus
Medicago caerulea var.	Citrus enation - woody gall
pauciflora; *Medicago*	(?) luteovirus
karatschaica; *Medicago lavrenkoi*;	Prunus necrotic ringspot
Medicago pauciflora; *Medicago*	ilarvirus
sativa var. *pilifera*	Rose (?) tobamovirus
Susceptible to:	Strawberry latent ringspot
Alfalfa 1 alphacryptovirus	(?) nepovirus
Alfalfa 2 (?) betacryptovirus	*Rubus fruticosus*
Alfalfa mosaic alfamovirus	Synonyms:
Bean leaf roll luteovirus	*Rubus plicatus*; *Rubus*
Bean yellow mosaic	*affinis*
potyvirus	Common names:
Beet curly top	Blackberry; Bramble;
hybrigeminivirus	European blackberry
Broad bean mottle	Susceptible to:
bromovirus	Black raspberry necrosis
Carnation mottle	virus
carmovirus	Raspberry leaf curl (?)
Carrot mosaic (?) potyvirus	luteovirus
Cassia mild mosaic (?)	Strawberry latent ringspot
carlavirus	(?) nepovirus
Chickpea distortion mosaic	*Rubus idaeus*
potyvirus	Synonyms:
Clover yellow mosaic	*Rubus buschii*; *Rubus*
potexvirus	*idaeus* var. *vulgatus*; *Rubus*
Clover yellow vein	*vulgatus* var. *buschii*
potyvirus	Common names:
Cucumber mosaic	European red raspberry;
cucumovirus	Red raspberry
Lucerne Australian latent	Susceptible to
nepovirus	Arabis mosaic nepovirus
Lucerne Australian	Black raspberry necrosis
symptomless (?) nepovirus	virus
Lucerne enation (?)	Cherry leaf roll nepovirus
nucleorhabdovirus	Cole latent (?) carlavirus
Lucerne transient streak	Raspberry bushy dwarf
sobemovirus	idaeovirus
Milk vetch dwarf nanavirus	Raspberry leaf curl (?)
Narcissus mosaic potexvirus	luteovirus
Pea enation mosaic	Raspberry ringspot
enamovirus	nepovirus
Pea seed-borne mosaic	Raspberry vein chlorosis (?)
potyvirus	nucleorhabdovirus
Pea streak carlavirus	Rubus yellow net (?)
Peanut stunt cucumovirus	badnavirus
Red clover mottle	Strawberry latent ringspot
comovirus	(?) nepovirus
Red clover necrotic mosaic	Thimbleberry ringspot virus
dianthovirus	Tomato ringspot nepovirus
Red clover vein mosaic	*Citrus limon*
carlavirus	Synonyms:
Subterranean clover stunt	*Citrus limonum*; *Citrus*
nanavirus	*medica* var. *limon*
Tobacco ringspot nepovirus	Common names:
Tobacco streak ilarvirus	Lemon; Limonero;
Tobacco yellow dwarf	Limoniere; Citronnier;
monogeminivirus	Zitronenbaum
Watermelon mosaic 2	Susceptible to:
potyvirus	Citrus enation - woody gall
White clover mosaic	(?) luteovirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
potexvirus	Citrus leaf rugose ilarvirus
Melilotus albus	Citrus ringspot virus
Synonyms:	Citrus tatter leaf capillovirus
Melilotus albus var. *annuus*;	Citrus tristeza closterovirus
Melilotus leucanthus	Citrus variegation ilarvirus
Common names:	*Citrus paradisi*
White sweet-clover; White	Common names:
melilot; Hubam	Grapefruit; Pomelo; Toronja
Susceptible to:	Susceptible to:
Alfalfa mosaic alfamovirus	Citrus enation - woody gall
Apple mosaic ilarvirus	(?) luteovirus
Bean common mosaic	Citrus leaf rugose ilarvirus
potyvirus	Citrus ringspot virus
Bean yellow mosaic	Citrus tristeza closterovirus
potyvirus	Pepper veinal mottle
Beet curly top	potyvirus
hybrigeminivirus	*Citrus sinensis*
Broad bean mottle	Synonyms:
bromovirus	*Citrus aurantium* var.
Broad bean necrosis	*sinensis*; *Citrus macracantha*
furovirus	Common names:
Broad bean stain comovirus	Sweet orange; Naranja
Broad bean true mosaic	Susceptible to:
comovirus	Citrus enation - woody gall
Clover yellow mosaic	(?) luteovirus
potexvirus	Citrus leaf rugose ilarvirus
Clover yellow vein	Citrus leprosis (?)
potyvirus	rhabdovirus
Cucumber mosaic	Citrus ringspot virus
cucumovirus	Citrus tatter leaf capillovirus
Galinsoga mosaic	Citrus tristeza closterovirus
carmovirus	*Sambucus canadensis*
Milk vetch dwarf nanavirus	Common names:
Muskmelon vein necrosis	American elder; American
carlavirus	elderberry; Sweet elder
Pea enation mosaic	Susceptible to:
enamovirus	Elderberry carlavirus
Pea mild mosaic comovirus	Elderberry latent (?)
Pea streak carlavirus	carmovirus
Peanut clump furovirus	*Dodonaea viscosa*
Peanut stunt cucumovirus	Common names:
Plum pox potyvirus	Hop shrub
Prune dwarf ilarvirus	Susceptible to:
Prunus necrotic ringspot	Dodonaea yellows-
ilarvirus	associated virus
Red clover mottle	*Antirrhinum majus*
comovirus	Common names:
Red clover vein mosaic	Snapdragon
carlavirus	Susceptible to:
Subterranean clover stunt	Alfalfa mosaic alfamovirus
nanavirus	Arabis mosaic nepovirus
Sweet clover latent (?)	Asystasia gangetica mottle
nucleorhabdovirus	(?) potyvirus
Sweet clover necrotic	Broad bean wilt fabavirus
mosaic dianthovirus	Carnation mottle
Tobacco etch potyvirus	carmovirus
Tobacco rattle tobravirus	Carnation ringspot
Tobacco ringspot nepovirus	dianthovirus
Tobacco streak ilarvirus	Cherry leaf roll nepovirus
Turnip mosaic potyvirus	Clover yellow vein
Watermelon mosaic 2	potyvirus
potyvirus	Cowpea mosaic comovirus
White clover mosaic	Cucumber mosaic
potexvirus	cucumovirus
Trifolium dubium	Cymbidium ringspot
Synonyms:	tombusvirus
Trifolium filiforme var.	Dogwood mosaic (?)
dubium; *Trifolium minus*;	nepovirus
Trifolium parviflorum; *Trifolium*	Elm mottle ilarvirus
procumbens	Groundnut eyespot
Common names:	potyvirus
Small hop clover; Suckling	Maracuja mosaic (?)
clover; Lesser yellow trefoil; Low	tobamovirus
hop clover; Yellow clover;	Marigold mottle potyvirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Shamrock	Papaya mosaic potexvirus
Susceptible to:	Pea streak carlavirus
Alfalfa mosaic alfamovirus	Peanut clump furovirus
Bean leaf roll luteovirus	Pepper Moroccan
Peanut stunt cucumovirus	tombusvirus
Soybean dwarf luteovirus	Plantago mottle tymovirus
Subterranean clover stunt	Poplar mosaic carlavirus
nanavirus	Prune dwarf ilarvirus
WETLAND - RIPARIAN	Prunus necrotic ringspot
Agrostis alba	ilarvirus
Glyceria occidentalis	Red clover necrotic mosaic
Alopecurus arundinaceus	dianthovirus
Glyceria striata	Red clover vein mosaic
Alopecurus pratensis	carlavirus
Hordeum brachyantherum	Rubus Chinese seed-borne
Beckmannia syzigachne	(?) nepovirus
Phalaris arundinacea	Scrophularia mottle
Deschampsia caespitosa	tymovirus
Poa palustris	Soybean mild mosaic virus
WILDFLOWERS AND	Soybean mosaic potyvirus
FORBES	Spinach latent ilarvirus
Achillea millefolium	Strawberry latent ringspot
Lupinus albicalus	(?) nepovirus
Cheiranthus allionii	Tamus latent (?) potexvirus
Lupinus perennis	Tobacco necrosis necrovirus
Coreopsis lanceolata	Tobacco rattle tobravirus
Papaver rhoeas	Tobacco ringspot nepovirus
Echinacea purpurea	Tobacco streak ilarvirus
Ratibida columnaris	Tomato black ring
Eschscholtzia californica	nepovirus
Rudbeckia hirta	Tomato bushy stunt
Linum lewisii	tombusvirus
Lupinus luteus	Viola mottle potexvirus
Common names:	White clover mosaic
European yellow lupine;	potexvirus
Yellow lupine	*Scrophularia nodosa*
Susceptible to:	Common names:
Bean yellow mosaic	Figwort; Figwort herb
potyvirus	Susceptible to:
Clover yellow vein	Scrophularia mottle
potyvirus	tymovirus
Dogwood mosaic (?)	Capsicum annuum
nepovirus	Synonyms:
Peanut stunt cucumovirus	*Capsicum cordiforme*
Cheiranthus cheiri	Common names:
Synonyms:	Pimiento; Bell pepper;
Erysimum cheiri	Cayenne pepper; Chili pepper;
Common names:	Common garden pepper; Green
Wallflower	pepper; Mango pepper; Paprika
Susceptible to:	pepper
Alfalfa mosaic alfamovirus	Susceptible to:
Beet western yellows	Alfalfa mosaic alfamovirus
luteovirus	Bean distortion dwarf (?)
Chicory yellow mottle	bigeminivirus
nepovirus	Beet western yellows
Cucumber mosaic	luteovirus
cucumovirus	Cassia mild mosaic (?)
Tobacco rattle tobravirus	carlavirus
Tobacco ringspot nepovirus	Celery latent (?) potyvirus
Tomato spotted wilt	Chilli veinal mottle (?)
tospovirus	potyvirus
Turnip crinkle carmovirus	Chino del tomat,
Turnip mosaic potyvirus	bigeminivirus
Turnip yellow mosaic	Cucumber mosaic
tymovirus	cucumovirus
Coreopsis lanceolata	Datura distortion mosaic
Susceptible to:	potyvirus
Bidens mosaic potyvirus	Eggplant mosaic tymovirus
Papaver rhoeas	Eggplant mottled dwarf
Common names:	nucleorhabdovirus
Corn poppy; Shirley poppy;	Eggplant severe mottle (?)
Field poppy	potyvirus
Susceptible to:	Henbane mosaic potyvirus
Beet western yellows	Marigold mottle potyvirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
clostrovirus	Melon Ourmia ourmiavirus
Linum grandiflorum	Paprika mild mottle
Synonyms:	tobamovirus
Linum rubrum	Peanut stunt cucumovirus
Common names:	Pelargonium vein clearing (?)
Flowering flax	cytorhabdovirus
Susceptible to:	Pepper hausteco
Beet pseudo-yellows (?)	bigeminivirus
closterovirus	Pepper Indian mottle
Oat blue dwarf marafivirus	potyvirus
Linum usitatissimum	Pepper mild mosaic (?)
Synonyms:	potyvirus
Linum crepitans; *Linum humile*; *Linum usitatissimum* ssp. *transitorium*; *Linum usitatissimum* var. *humile*	Pepper mild mottle
	tobamovirus
	Pepper mild tigr, (?)
	bigeminivirus
Common names:	Pepper Moroccan
Flax; Linseed; Lino	tombusvirus
Susceptible to:	Pepper mottle potyvirus
Alfalfa mosaic alfamovirus	Pepper ringspot tobravirus
Beet curly top	Pepper severe mosaic
hybrigeminivirus	potyvirus
Beet pseudo-yellows (?)	Pepper Texas bigeminivirus
closterovirus	Pepper veinal mottle
Oat blue dwarf marafivirus	Potyvirus
Tobacco rattle tobravirus	Physalis mosaic tymovirus
ORNAMENTAL GRASSES	Pittosporum vein yellowing
Acorus Gramineus	nucleorhabdovirus
Acorus Calamus	Potato aucuba mosaic
Acorus Gramineus	potexvirus
Alopecurus Pratensis	Potato mop-top furovirus
Andropogon Scoparius	Potato Y potyvirus
Andropogon Gerardii	Red pepper 1 (?)
Arrhenatherum Elatius	alphacryptovirus
Arundo Formosana	Red pepper 2 (?)
Briza Media	alphacryptovirus
Calamagrostis Acutiflora	Ribgrass mosaic
Calamagrostis Arundinacea	tobamovirus
Calamagrostis Acutiflora	Serrano golden mosaic
Calamagrostis Acutiflora	bigeminivirus
Carex Glauca	Sweet potato ringspot (?)
Carex Siderostica	nepovirus
Carex Albula	Tobacco etch potyvirus
Carex Nigra	Tobacco leaf curl
Carex Muskingumensis	bigeminivirus
Carex Riparia	Tobacco mild green mosaic
Carex Evergold	tobamovirus
Carex Comans	Tobacco mosaic satellivirus
Cortaderia Selloana	Tobacco rattle tobravirus
Cortaderia Selloana Rosea	Tobacco streak ilarvirus
Deschampsia Cespitosa	Tomato bushy stunt
Elymus Arenarius	tombusvirus
Erianthus Ravennae	Tomato mosaic tobamovirus
Ovina Gigantea	Tomato Peru potyvirus
Ovina Glauca	Tomato spotted wilt
Glyceria Maxima	tospovirus
Hakonechloa Macra	*Lycopersicon esculentum*
Hakonechloa Macra	Common names:
Helictotrichon Sempervirens	Tomato; Tomate
Holcus Variegated	Susceptible to:
Hystrix Patula	Abelia latent tymovirus
Imperata Red Baron	Abutilon mosaic
Juncus Effusus	bigeminivirus
Juncus Ensifolius	Alfalfa mosaic alfamovirus
Juncus Filiformis	Arabis mosaic nepovirus
Juncus Inflexus	Arracacha A nepovirus
Koeleria Cristata	Arracacha B (?) nepovirus
Koeleria Glauca	Beet curly top
Luzula Sylvatica	hybrigeminivirus
Melica Ciliata	Beet western yellows
Melica Nutans	luteovirus
Miscanthus Sinensis	Blueberry leaf mottle
Molinia Caerulea	nepovirus
Virgatum Rotstrahlbusch	Brinjal mild mosaic (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Pennisetum Alopecuroides	potyvirus
Pennisetum Ruppelianum	Carnation mottle
Pennisetum Alopecuroides	carmovirus
Pennisetum Alopecuroides	Carrot mosaic (?) potyvirus
Pennisetum Alopecuroides	Cassava green mottle
Pennisetum Setaceum	nepovirus
Pennisetum Setaceum	Cassia mild mosaic (?)
Pennisetum Cassian	carlavirus
Phalaris Arundinacea	Chickpea chlorotic dwarf (?)
Phalaris Arundinacea	monogeminivirus
Phalaris Arundinacea	Chino del tomat,
Sesleria Autumnalis	bigeminivirus
Sesleria Caerulea	Clover wound tumor
Sporobolus Helerolepsis	phytoreovirus
Stipa Capillata	Commelina X potexvirus
Stipa Extremiorientalis	Cowpea mild mottle (?)
Stipa Gigantea	carlavirus
Stipa Tenuissima	Croton yellow vein mosaic
Stipa Grandis	bigeminivirus
Stipa Pennata	Cucumber mosaic
Stipa Ucrainica	cucumovirus
Impatiens	Cymbidium ringspot
Impatiens necrotic spot tospovirus	tombusvirus
Carnation mottle carmovirus	Datura distortion mosaic
Helenium S carlavirus	potyvirus
Impatiens latent (?) potexvirus	Datura innoxia Hungarian
Aster chlorotic stunt (?) carlavirus	mosaic (?) potyvirus
Dasheen mosaic potyvirus	Datura mosaic (?) potyvirus
Aglaonema	Datura necrosis potyvirus
Alocasia	Datura yellow vein
Amorphophallus	nucleorhabdovirus
Arisaema	Dogwood mosaic (?)
Caladium hortulanum	nepovirus
Chenopodium amaranticolor	Dulcamara mottle
Chenopodium ambrosioides	tymovirus
Chenopodium quinoa	Eggplant green mosaic
Colocasia esculenta	potyvirus
Cryptocoryne	Eggplant mosaic tymovirus
Cyrtosperma	Eggplant mottled dwarf
Dieffenbachia picta	nucleorhabdovirus
Nicotiana benthamiana	Eggplant severe mottle (?)
Philodendron selloum	potyvirus
Philodendron verrucosum	Elderberry latent (?)
Richardia	carmovirus
Saponaria vaccaria	Elm mottle ilarvirus
Spathiphyllum	Epirus cherry ourmiavirus
Tetragonia tetragonioides	Foxtail mosaic potexvirus
Xanthosoma caracu	Groundnut eyespot
Zantedeschia (no species name provided)	potyvirus
	Henbane mosaic potyvirus
Zantedeschia elliottiana	Lettuce necrotic yellows
Colocasia bobone disease (?)	cytorhabdovirus
rhabdovirus	Maracuja mosaic (?)
Dasheen bacilliform (?)	tobamovirus
badnavirus	Marigold mottle potyvirus
Dasheen mosaic potyvirus	Melilotus mosaic (?)
Colocasia esculenta	potyvirus
Konjak mosaic (?) potyvirus	Melon Ourmia ourmiavirus
Philodendron oxycardium	Nerine X potexvirus
	Okra leaf-curl bigeminivirus
Philodendron selloum	Ononis yellow mosaic
Abelia latent tymovirus	tymovirus
Abelia grandiflora	Parietaria mottle ilarvirus
Abelmoschus esculentus	Parsnip yellow fleck
Acer palmatum	sequivirus
Amaranthus caudatus	Pea streak carlavirus
Atropa belladonna	Peanut clump furovirus
Brassica campestris ssp. *pekinensis*	Peanut stunt cucumovirus
	Pelargonium line pattern (?)
Catharanthus roseus	carmovirus
Celosia argentea	Pelargonium zonate spot
Chenopodium amaranticolor	ourmiavirus
Chenopodium murale	Pepino mosaic potexvirus
Chenopodium quinoa	Pepper Indian mottle

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Datura metel	potyvirus
Datura stramonium	Pepper mild tigr, (?)
Glycine max	bigeminivirus
Gomphrena globosa	Pepper Moroccan
Gossypium hirsutum	tombusvirus
Hordeum vulgare	Pepper mottle potyvirus
Lobelia erinus	Pepper ringspot tobravirus
Lycopersicon esculentum	Pepper severe mosaic
Momordica balsamina	potyvirus
Nicotiana clevelandii	Pepper Texas bigeminivirus
Nicotiana glutinosa	Pepper veinal mottle
Nicotiana rustica	potyvirus
Petunia x *hybrida*	Physalis mosaic tymovirus
Physalis peruviana	Pittosporum vein yellowing
Sesamum indicum	nucleorhabdovirus
Solanum melongena	Plantain X potexvirus
Solanum tuberosum	Plum pox potyvirus
Tetragonia tetragonioides	Potato 14R (?) tobamovirus
Tithonia speciosa	Potato Andean latent
Torenia fournieri	tymovirus
Vicia faba	Potato Andean mottle
Allium	comovirus
Susceptible to:	Potato aucuba mosaic
Onion yellow dwarf	potexvirus
potyvirus	Potato black ringspot
Allium ampeloprasum var.	nepovirus
holmense	Potato leafroll luteovirus
Garlic common latent (?)	Potato M carlavirus
carlavirus	Potato mop-top furovirus
Allium ampeloprasum var.	Potato U nepovirus
sectivum	Potato V potyvirus
Susceptible to:	Potato Y potyvirus
Sint-Jan's onion latent (?)	Potato yellow mosaic
carlavirus	bigeminivirus
Allium cepa	Raspberry ringspot
Synonyms:	nepovirus
Allium ascalonicum; *Allium*	Red clover necrotic mosaic
cepa var. *aggregatum*; *Allium*	dianthovirus
cepa var. *solaninum*	Ribgrass mosaic
Common names:	tobamovirus
Onion; Shallot; Tama-negi;	Rose (?) tobamovirus
Eschalot; Potato onion; Multiplier	Rubus Chinese seed-borne (?)
onion; Cebolla; Spanish onion	nepovirus
Susceptible to:	Serrano golden mosaic
Leek yellow stripe potyvirus	bigeminivirus
Onion mite-borne latent (?)	Solanum apical leaf curling (?)
potexvirus	bigeminivirus
Onion yellow dwarf	Soybean crinkle leaf (?)
potyvirus	bigeminivirus
Pepper venial mottle	Soybean mild mosaic virus
potyvirus	Strawberry latent ringspot (?)
Shallot latent carlavirus	nepovirus
Shallot mite-borne latent (?)	Sunflower ringspot (?)
potexvirus	ilarvirus
Shallot yellow stripe (?)	Sweet potato mild mottle
potyvirus	ipomovirus
Sint-Jan's onion latent (?)	Tamarillo mosaic potyvirus
carlavirus	Tamus latent (?) potexvirus
Tobacco rattle tobravirus	Tobacco etch potyvirus
Welsh onion yellow stripe (?)	Tobacco leaf curl
potyvirus	bigeminivirus
Amaranthaceae	Tobacco mild green mosaic
Susceptible to:	tobamovirus
Apple stem grooving	Tobacco mosaic satellivirus
capillovirus	Tobacco mosaic
Insusceptible to:	tobamovirus
Voandzeia necrotic mosaic	Tobacco mottle umbravirus
tymovirus	Tobacco necrosis necrovirus
Amaranthus bicolor	Tobacco necrotic dwarf
Insusceptible to:	luteovirus
Onion mite-borne latent (?)	Tobacco rattle tobravirus
potexvirus	Tobacco ringspot nepovirus
Amaranthus caudatus	Tobacco streak ilarvirus
Synonyms:	Tobacco stunt varicosavirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Amaranthus caudatus ssp.	Tobacco vein-distorting (?)
mantegazzianus; *Amaranthus*	luteovirus
caudatus var. *alopecurus*;	Tobacco vein mottling
Amaranthus dussii; *Amaranthus*	potyvirus
edulis; *Amaranthus*	Tobacco yellow dwarf
mantegazzianus	monogeminivirus
Common names:	Tobacco yellow net (?)
Inca wheat; Love-lies-	luteovirus
bleeding; Tassel-flower; Kiwichi;	Tobacco yellow vein
Coimi	assistor (?) luteovirus
Susceptible to:	Tobacco yellow vein (?)
Abelia latent tymovirus	umbravirus
Alfalfa mosaic alfamovirus	Tomato aspermy
Amaranthus leaf mottle	cucumovirus
potyvirus	Tomato Australian leafcurl
Amaranthus mosaic (?)	bigeminivirus
potyvirus	Tomato black ring
Arracacha A nepovirus	nepovirus
Arracacha B (?) nepovirus	Tomato bushy stunt
Bean yellow mosaic	tombusvirus
potyvirus	Tomato chlorotic spot (?)
Beet curly top	tospovirus
hybrigeminivirus	Tomato golden mosaic
Beet mosaic potyvirus	bigeminivirus
Cactus X potexvirus	Tomato infectious chlorosis (?)
Carnation mottle	closterovirus
carmovirus	Tomato mild mottle (?)
Carnation ringspot	potyvirus
dianthovirus	Tomato mosaic tobamovirus
Carnation vein mottle	Tomato mottle
potyvirus	bigeminivirus
Celery latent (?) potyvirus	Tomato Peru potyvirus
Chicory yellow mottle	Tomato pseudo curly top (?)
nepovirus	hybrigeminivirus
Clover yellow mosaic	Tomato ringspot nepovirus
potexvirus	Tomato spotted wilt
Clover yellow vein	tospovirus
potyvirus	Tomato top necrosis (?)
Cucumber mosaic	nepovirus
cucumovirus	Tomato vein clearing
Cymbidium ringspot	nucleorhabdovirus
tombusvirus	Tomato yellow leaf curl
Dahlia mosaic caulimovirus	bigeminivirus
Elderberry carlavirus	Tomato yellow mosaic
Grapevine fanleaf nepovirus	bigeminivirus
Heracleum latent trichovirus	Tulip chlorotic blotch
Humulus japonicus ilarvirus	potyvirus
Iris fulva mosaic potyvirus	Tulip X potexvirus
Lamium mild mottle	Turnip crinkle carmovirus
fabavirus	Ullucus mild mottle
Lettuce mosaic potyvirus	tobamovirus
Maclura mosaic	White clover mosaic
macluravirus	potexvirus
Marigold mottle potyvirus	Wild potato mosaic
Peanut stunt cucumovirus	potyvirus
Plantain X potexvirus	Wineberry latent virus
Potato 14R (?) tobamovirus	*Nicotiana benthamiana*
Potato Andean latent	Susceptible to:
tymovirus	Ahlum waterborne (?)
Potato black ringspot	carmovirus
nepovirus	Alstroemeria (?) ilarvirus
Potato leafroll luteovirus	Alstroemeria mosaic
Red clover necrotic mosaic	potyvirus
dianthovirus	Alstroemeria streak (?)
Ribgrass mosaic	potyvirus
tobamovirus	Amazon lily mosaic (?)
Telfairia mosaic potyvirus	potyvirus
Tobacco etch potyvirus	Apple mosaic ilarvirus
Tobacco necrosis necrovirus	Arracacha Y potyvirus
Tobacco rattle tobravirus	Artichoke latent potyvirus
Tobacco ringspot nepovirus	Artichoke latent S (?)
Tobacco streak ilarvirus	carlavirus
Tomato black ring	Artichoke mottled crinkle
nepovirus	tombusvirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Tomato spotted wilt tospovirus	Artichoke vein banding (?) nepovirus
Turnip mosaic potyvirus	Asparagus 3 potexvirus
Ullucus mild mottle tobamovirus	Asystasia gangetica mottle (?) potyvirus
Viola mottle potexvirus	Barley yellow streak mosaic virus
Watermelon mosaic 2 potyvirus	Bean calico mosaic bigeminivirus
Zygocactus Montana X (?) potexvirus	Bean common mosaic potyvirus
Amaranthus tricolor	Beet curly top hybrigeminivirus
Synonyms:	Blueberry leaf mottle nepovirus
Amaranthus gangeticus; *Amaranthus gangeticus* var. *melancholicus*; *Amaranthus mangostanus*; *Amaranthus polygamus*; *Amaranthus tricolor* ssp. *mangostanus;* *Amaranthus tricolor* ssp. *tristis*	Blueberry necrotic shock ilarvirus
	Caper latent carlavirus
	Caraway latent (?) nepovirus
Common names:	Carrot mottle mimic umbravirus
Chinese amaranth; Tampala; Ganges amaranth	Carrot mottle umbravirus
Susceptible to:	Carrot yellow leaf (?) closterovirus
Amaranthus leaf mottle potyvirus	Cassava African mosaic bigeminivirus
Amaranthus mosaic (?) potyvirus	Cassava brown streak-associated (?) carlavirus
Apple mosaic ilarvirus	Cassava brown streak potyvirus
Amaryllis	Cassava Caribbean mosaic (?) potexvirus
Susceptible to:	Cassava Colombian symptomless (?) potexvirus
Amaryllis (?) alphacryptovirus	Cassava common mosaic (?) potexvirus
Narcissus	Cassava green mottle nepovirus
Susceptible to:	Cassava Indian mosaic bigeminivirus
Narcissus yellow stripe potyvirus	Cassava Ivorian bacilliform ourmiavirus
Insusceptible to:	Cassava X potexvirus
Silene X (?) potexvirus	Cherry leaf roll nepovirus
Narcissus jonquilla	Chickpea bushy dwarf potyvirus
Common names:	Chickpea chlorotic dwarf (?) monogeminivirus
Jonquil	Chickpea distortion mosaic potyvirus
Susceptible to:	Chicory yellow mottle nepovirus
Strawberry latent ringspot (?) nepovirus	Chino del tomat, bigeminivirus
Insusceptible to:	Citrus ringspot virus
Ornithogalum mosaic potyvirus	Cowpea chlorotic mottle bromovirus
Narcissus poeticus	Croton yellow vein mosaic bigeminivirus
Common names:	Cucumber necrosis tombusvirus
Narcissus; Pheasant's-eye; Poet's narcissus	Cymbidium ringspot tombusvirus
Susceptible to:	Cynara (?) nucleorhabdovirus
Narcissus tip necrosis (?) carmovirus	Dandelion yellow mosaic sequivirus
Raspberry ringspot nepovirus	Dasheen mosaic potyvirus
Tobacco rattle tobravirus	Desmodium mosaic potyvirus
Tomato black ring nepovirus	Dioscorea green banding mosaic potyvirus
Yucca	Dioscorea latent (?)
Susceptible to:	
Furcraea necrotic streak (?)	

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
dianthovirus	potexvirus
Chlorophytum comosum	Dogwood mosaic (?) nepovirus
Common names:	Eggplant green mosaic potyvirus
Spider plant; Spider-ivy; Ribbon plant	Eggplant mottled dwarf nucleorhabdovirus
Insusceptible to:	Eggplant severe mottle (?) potyvirus
Onion mite-borne latent (?) potexvirus	Elderberry latent (?) carmovirus
Shallot mite-borne latent (?) potexvirus	Epirus cherry ourmiavirus
Sint-Jan's onion latent (?) carlavirus	Euphorbia mosaic bigeminivirus
Tradescantia-Zebrina potyvirus	Grapevine A (?) trichovirus
Catharanthus roseus	Grapevine Algerian latent tombusvirus
Synonyms:	Grapevine Bulgarian latent nepovirus
Ammocallis rosea; *Lochnera rosea*; *Vinca rosea*	Grapevine chrome mosaic nepovirus
Common names:	Grapevine fanleaf nepovirus
Bright-eyes; Madagascar periwinkle; Old-maid; Rose periwinkle; Rosy periwinkle	Groundnut chlorotic spot (?) potexvirus
Susceptible to:	Groundnut rosette umbravirus
Abelia latent tymovirus	Hibiscus latent ringspot nepovirus
Alfalfa mosaic alfamovirus	Hydrangea mosaic ilarvirus
Apple mosaic ilarvirus	Ivy vein clearing (?) cytorhabdovirus
Bean pod mottle comovirus	Kalanchoe isometric virus
Beet curly top hybrigeminivirus	Lato River tombusvirus
Belladonna mottle tymovirus	Lettuce big-vein varicosavirus
Cacao yellow mosaic tymovirus	Lettuce mosaic potyvirus
Carnation mottle carmovirus	Lilac chlorotic leafspot capillovirus
Cassava green mottle nepovirus	Lily X potexvirus
Cherry leaf roll nepovirus	Lucerne Australian symptomless (?) nepovirus
Citrus leaf rugose ilarvirus	Maracuja mosaic (?) tobamovirus
Citrus ringspot virus	Melon Ourmia ourmiavirus
Clover wound tumor phytoreovirus	Melothria mottle (?) potyvirus
Clover yellow mosaic potexvirus	Nandina mosaic (?) potexvirus
Cowpea severe mosaic comovirus	Narcissus latent macluravirus
Cucumber mosaic cucumovirus	Narcissus tip necrosis (?) carmovirus
Dogwood mosaic (?) nepovirus	Neckar River tombusvirus
Dulcamara mottle tymovirus	Nerine potyvirus
Elm mottle ilarvirus	Nicotiana velutina mosaic (?) furovirus
Erysimum latent tymovirus	Oat golden stripe furovirus
Foxtail mosaic potexvirus	Okra mosaic tymovirus
Humulus japonicus ilarvirus	Olive latent 1 (?) sobemovirus
Lilac ring mottle ilarvirus	Olive latent 2 (?) ourmiavirus
Nandina mosaic (?) potexvirus	Paprika mild mottle tobamovirus
Narcissus mosaic potexvirus	Parsnip yellow fleck sequivirus
Okra mosaic tymovirus	Passiflora ringspot potyvirus
Pea seed-borne mosaic potyvirus	Peanut chlorotic streak caulimovirus
Peach enation (?) nepovirus	Peanut clump furovirus
Peanut stunt cucumovirus	Peanut green mosaic potyvirus
Pepper ringspot tobravirus	Peanut yellow spot
Pepper veinal mottle potyvirus	
Plum American line pattern ilarvirus	
Poplar mosaic carlavirus	
Potato 14R (?) tobamovirus	
Potato black ringspot nepovirus	

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Potato T trichovirus	tospovirus
Prune dwarf ilarvirus	Pelargonium vein clearing (?)
Prunus necrotic ringspot	cytorhabdovirus
ilarvirus	Pepper Moroccan
Scrophularia mottle	tombusvirus
tymovirus	Pepper mottle potyvirus
Spring beauty latent	Pepper ringspot tobravirus
bromovirus	Pepper Texas bigeminivirus
Tobacco mosaic satellivirus	Pepper veinal mottle
Tobacco necrosis necrovirus	potyvirus
Tobacco rattle tobravirus	Physalis mosaic tymovirus
Tobacco ringspot nepovirus	Pittosporum vein yellowing
Tobacco streak ilarvirus	nucleorhabdovirus
Tobacco stunt varicosavirus	Plantain 6 (?) carmovirus
Tomato spotted wilt	Plantain 7 (?) potyvirus
tospovirus	Plantain X potexvirus
Tulare apple mosaic	Plum American line pattern
ilarvirus	ilarvirus
Turnip crinkle carmovirus	Plum pox potyvirus
Watermelon mosaic 2	Poinsettia mosaic (?)
potyvirus	tymovirus
Wild cucumber mosaic	Potato 14R (?) tobamovirus
tymovirus	Potato Andean latent
Hedera helix	tymovirus
Common names:	Potato Andean mottle
English ivy	comovirus
Susceptible to:	Potato black ringspot
Ivy vein clearing (?)	nepovirus
cytorhabdovirus	Potato mop-top furovirus
sparagus officinalis	Potato T trichovirus
Synonyms:	Prune dwarf ilarvirus
Asparagus longifolius	Prunus necrotic ringspot
Common names:	ilarvirus
Garden asparagus;	Red clover necrotic mosaic
Asparagus; Esparrag	dianthovirus
Susceptible to:	Rice stripe necrosis (?)
Arabis mosaic nepovirus	furovirus
Asparagus 1 potyvirus	Rubus Chinese seed-borne (?)
Asparagus 2 ilarvirus	nepovirus
Strawberry latent ringspot (?)	Silene X (?) potexvirus
nepovirus	Sitke waterborne (?)
Tobacco streak ilarvirus	tombusvirus
Dryopteris filix-mas	Solanum apical leaf curling (?)
Common names:	bigeminivirus
Male fern	Solanum nodiflorum mottle
Susceptible to:	sobemovirus
Fern (?) potyvirus	Sonchus yellow net
Polystichum falcatum	nucleorhabdovirus
Susceptible to:	Soybean mosaic potyvirus
Harts tongue fern (?)	Sweet potato feathery
tobravirus	mottle potyvirus
Phyllitis scolopendrium	Sweet potato latent (?)
Synonyms:	potyvirus
Asplenium scolopendrium	Sweet potato mild mottle
Common names:	ipomovirus
Hart's-tongue fern	Sweet potato ringspot (?)
Susceptible to:	nepovirus
Harts tongue fern (?)	Sweet potato sunken vein (?)
tobravirus	closterovirus
Aucuba japonica	Tamus latent (?) potexvirus
Synonyms:	Telfairia mosaic potyvirus
Aucuba japonica var.	Tobacco mosaic satellivirus
variegata	Tobacco mosaic
Common names:	tobamovirus
Spotted-laurel; Japanese-	Tobacco rattle tobravirus
laurel	Tobacco streak ilarvirus
Susceptible to:	Tobacco stunt varicosavirus
Aucuba ringspot (?)	Tomato Australian leafcurl
badnavirus	bigeminivirus
Cycas necrotic stunt	Tomato bushy stunt
nepovirus	tombusvirus
Begonia elatior	Tomato golden mosaic
Susceptible to:	bigeminivirus
Carnation mottle	Tomato mild mottle (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
carmovirus	potyvirus
Begonia x *tuberhybrida*	Tomato mosaic tobamovirus
Common names:	Tomato mottle
Hybris tuberous begonia	bigeminivirus
Insusceptible to:	Tomato ringspot nepovirus
Aster chlorotic stunt (?)	Tomato yellow leaf curl
carlavirus	bigeminivirus
Catalpa bignonioides	Tomato yellow mosaic
Synonyms:	bigeminivirus
Catalpa bignonioides f.	Tropaeolum 1 potyvirus
aurea	Tropaeolum 2 potyvirus
Common names:	Tulip chlorotic blotch
Catawba; Common catalpa;	potyvirus
Indian-bean; Southern catalpa;	Tulip halo necrosis (?) virus
Cigartree; Smoking-bean	Tulip X potexvirus
Susceptible to:	Ullucus mild mottle
Scrophularia mottle	tobamovirus
tymovirus	Ullucus mosaic potyvirus
Acer palmatum	Vanilla necrosis potyvirus
Abelia latent tymovirus	Watercress yellow spot
Betula	virus
Susceptible to:	Watermelon mosaic 2
Cherry leaf roll nepovirus	potyvirus
Ceiba pentandra	Weddel waterborne (?)
Synonyms:	carmovirus
Bombax pentandrum; *Ceiba*	Wild potato mosaic
casearia; *Eriodendron*	potyvirus
anfractuosum	Yam mosaic potyvirus
Common names:	*Nicotiana tabacum*
Ceiba; Kapok; Silk-cotton-	Synonyms:
tree; White silk-cotton-tree;	*Nicotiana chinensis*;
Kapokbaum; Kapokier; Arbe-	*Nicotiana tabacum* var.
kapok	*macrophylla*
Susceptible to:	Common names:
Cacao swollen shoot	Tobacco
badnavirus	Susceptible to:
Cacao yellow mosaic	Abutilon mosaic
tymovirus	bigeminivirus
Okra mosaic tymovirus	Alfalfa mosaic alfamovirus
Myosotis sylvatica	Alstroemeria (?) ilarvirus
Synonyms:	Alstroemeria mosaic
Myosotis alpestris;	potyvirus
Myosotis oblongata	Amaranthus leaf mottle
Common names:	potyvirus
Garden forget-me-not;	Arabis mosaic nepovirus
Wood forget-me-not	Arracacha A nepovirus
Susceptible to:	Arracacha B (?) nepovirus
Arabis mosaic nepovirus	Arracacha Y potyvirus
Carnation ringspot	Artichoke Italian latent
dianthovirus	nepovirus
Cymbidium ringspot	Artichoke yellow ringspot
tombusvirus	nepovirus
Tobacco rattle tobravirus	Asparagus 2 ilarvirus
Tobacco ringspot nepovirus	Asparagus 3 potexvirus
Tomato black ring	Asystasia gangetica mottle
nepovirus	(?) potyvirus
Ananas comosus	Barley stripe mosaic
Synonyms:	hordeivirus
Ananas duckei; *Ananas*	Bean distortion dwarf (?)
sativus; *Ananas sativus* var.	bigeminivirus
duckei; *Bromelia ananas*;	Bean yellow mosaic
Bromelia comosa	potyvirus
Common names:	Beet curly top
Pineapple; Pina	hybrigeminivirus
Susceptible to:	Beet pseudo-yellows (?)
Pineapple chlorotic leaf	closterovirus
streak (?) nucleorhabdovirus	Belladonna mottle
Pineapple wilt-associated	tymovirus
(?) closterovirus	Bidens mosaic potyvirus
Tomato spotted wilt	Blueberry leaf mottle
tospovirus	nepovirus
Buxus sempervirens	Blueberry necrotic shock
Synonyms:	ilarvirus
Buxus colchica	Bramble yellow mosaic (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Common names:	potyvirus
Boxwood; Common	Broad bean wilt fabavirus
boxwood; Turkish boxwood	Burdock yellow mosaic (?)
Susceptible to:	potexvirus
Arabis mosaic nepovirus	Cacao necrosis nepovirus
Cactaceae family	Cacao yellow mosaic
Including:	tymovirus
Austrocylindropuntia cylindrica	Carnation ringspot
Cactaceae	dianthovirus
Carnegiea gigantea (syn. *Cereus giganteus*)	Cassava African mosaic bigeminivirus
Saguaro; Giant cactus	Cassava green mottle
Cereus	nepovirus
Chamaecereus sylvestrii	Cassava Indian mosaic
Echinocereus procumbens	bigeminivirus
Echinopsis	Cassava Ivorian bacilliform
Epiphyllum	ourmiavirus
Ferocactus acanthodes (syn. *Echinocactus acanthodes)*	Cassia mild mosaic (?) carlavirus
Opuntia engelmannii	Cassia severe mosaic (?)
Opuntia vulgaris (syn. *Cactus monacanthos*; *Opuntia monacantha)*	closterovirus Celery latent (?) potyvirus
Prickly-pear cactus; Tuna;	Cherry leaf roll nepovirus
Prickly-pear; Drooping prickly-pear	Chickpea chlorotic dwarf (?) monogeminivirus
Pereskia saccharosa	Chicory yellow mottle
Schlumbergera bridgesii	nepovirus
Zygocactus	Chilli veinal mottle (?) potyvirus
Zygocactus truncatus	Chino del tomat,
Zygocactus x Schlumbergera	bigeminivirus
Susceptible to:	Citrus ringspot virus
Cactus X potexvirus	Clover wound tumor
Cactus 2 carlavirus	phytoreovirus
Lobelia erinus	Clover yellow vein
Common names:	potyvirus
Edging lobelia	Commelina X potexvirus
Susceptible to:	Cowpea chlorotic mottle
Abelia latent tymovirus	bromovirus
Arabis mosaic nepovirus	Cowpea mosaic comovirus
Carnation ringspot	Cowpea mottle (?)
dianthovirus	carmovirus
Cherry leaf roll nepovirus	Cowpea severe mosaic
Elm mottle ilarvirus	comovirus
Peanut stunt cucumovirus	Croton yellow vein mosaic
Strawberry latent ringspot	bigeminivirus
(?) nepovirus	Cucumber green mottle
Tobacco rattle tobravirus	mosaic tobamovirus
Tomato black ring	Cucumber mosaic
nepovirus	cucumovirus
Humulus japonicus	Cucumber necrosis
Synonyms:	tombusvirus
Humulus scandens	Cymbidium ringspot
Common names:	tombusvirus
Japanese hop	Datura Colombian potyvirus
Susceptible to:	Datura distortion mosaic
Hop latent carlavirus	potyvirus
Humulus japonicus ilarvirus	Datura innoxia Hungarian
Lonicera	mosaic (?) potyvirus
Susceptible to:	Datura mosaic (?) potyvirus
Eggplant mottled dwarf	Datura necrosis potyvirus
nucleorhabdovirus	Datura shoestring potyvirus
Pittosporum vein yellowing	Datura yellow vein
nucleorhabdovirus	nucleorhabdovirus
Insusceptible to:	Dioscorea latent (?)
Tomato yellow leaf curl	potexvirus
bigeminivirus	Dogwood mosaic (?)
Lonicera americana	nepovirus
Susceptible to:	Eggplant green mosaic
Honeysuckle latent	potyvirus
carlavirus	Eggplant mild mottle (?)
Carica papaya	carlavirus
Synonyms:	Eggplant mottled crinkle
Carica peltata; *Carica*	tombusvirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
posoposa; *Papaya carica*	Eggplant mottled dwarf
Common names:	nucleorhabdovirus
Papaya; Pawpaw	Eggplant severe mottle (?)
Susceptible to:	potyvirus
Croton yellow vein mosaic	Elderberry latent (?)
bigeminivirus	carmovirus
Papaya mosaic potexvirus	Elm mottle ilarvirus
Papaya ringspot potyvirus	Epirus cherry ourmiavirus
Watermelon mosaic 1	Eucharis mottle (?)
potyvirus	nepovirus
Dianthus barbatus	Foxtail mosaic potexvirus
Common names:	Frangipani mosaic
Sweet William	tobamovirus
Susceptible to:	Galinsoga mosaic
Alfalfa mosaic alfamovirus	carmovirus
Arabis mosaic nepovirus	Grapevine Bulgarian latent
Beet curly top	nepovirus
hybrigeminivirus	Grapevine chrome mosaic
Beet mosaic potyvirus	nepovirus
Carnation latent carlavirus	Grapevine fanleaf nepovirus
Carnation mottle	Guar top necrosis virus
carmovirus	Henbane mosaic potyvirus
Carnation necrotic fleck	Hibiscus latent ringspot
closterovirus	nepovirus
Carnation (?) rhabdovirus	Hippeastrum mosaic
Carnation ringspot	potyvirus
dianthovirus	Hop American latent
Carnation vein mottle	carlavirus
potyvirus	Humulus japonicus ilarvirus
Carnation yellow stripe (?)	Ivy vein clearing (?)
necrovirus	cytorhabdovirus
Clover wound tumor	Kalanchoe isometric virus
phytoreovirus	Kyuri green mottle mosaic
Melon Ourmia ourmiavirus	tobamovirus
Okra mosaic tymovirus	Lamium mild mottle
Peanut stunt cucumovirus	fabavirus
Pelargonium line pattern (?)	Lilac chlorotic leafspot
carmovirus	capillovirus
Potato black ringspot	Lilac ring mottle ilarvirus
nepovirus	Lisianthus necrosis (?)
Potato M carlavirus	necrovirus
Silene X (?) potexvirus	Lucerne Australian latent
Strawberry latent ringspot (?)	nepovirus
(?) nepovirus	Lucerne Australian
Tobacco ringspot nepovirus	symptomless (?) nepovirus
Tomato bushy stunt	Lucerne transient streak
tombusvirus	sobemovirus
Viola mottle potexvirus	Lychnis ringspot
Dianthus caryophyllus	hordeivirus
Common names:	Maclura mosaic
Carnation; Clavel	macluravirus
Susceptible to:	Maracuja mosaic (?)
Alfalfa mosaic alfamovirus	tobamovirus
Arabis mosaic nepovirus	Marigold mottle potyvirus
Beet curly top	Melandrium yellow fleck
hybrigeminivirus	bromovirus
Carnation 1	Melilotus mosaic (?)
alphacryptovirus	potyvirus
Carnation 2 (?)	Melon Ourmia ourmiavirus
alphacryptovirus	Milk vetch dwarf nanavirus
Carnation etched ring	Myrobalan latent ringspot
caulimovirus	nepovirus
Carnation Italian ringspot	Narcissus latent
tombusvirus	macluravirus
Carnation latent carlavirus	Neckar River tombusvirus
Carnation mottle	Nerine potyvirus
carmovirus	Nicotiana velutina mosaic (?)
Carnation necrotic fleck	furovirus
Closterovirus	Odontoglossum ringspot
Carnation (?) rhabdovirus	tobamovirus
Carnation ringspot	Okra leaf-curl bigeminivirus
dianthovirus	Olive latent 1 (?)
Carnation vein mottle	sobemovirus
Potyvirus	Olive latent 2 (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Carnation yellow stripe (?) necrovirus	ourmiavirus
Lettuce infectious yellows (?) closterovirus	Orchid fleck (?) rhabdovirus
Melandrium yellow fleck bromovirus	Paprika mild mottle tobamovirus
Potato M carlavirus	Parietaria mottle ilarvirus
Tobacco stunt varicosavirus	Parsnip yellow fleck sequivirus
Gypsophila elegans	Passionfruit woodiness potyvirus
Common names:	Patchouli mosaic potyvirus
Baby's-breath	Pea early browning
Susceptible to:	tobravirus
Belladonna mottle tymovirus	Pea mosaic potyvirus
Lychnis ringspot hordeivirus	Pea streak carlavirus
Tobacco etch potyvirus	Peach enation (?) nepovirus
Tobacco necrosis necrovirus	Peach rosette mosaic nepovirus
Tobacco rattle tobravirus	Peanut chlorotic streak caulimovirus
Tobacco ringspot nepovirus	Peanut clump furovirus
Tomato bushy stunt tombusvirus	Peanut stunt cucumovirus
Euonymus europaeus	Pelargonium line pattern (?) carmovirus
Synonyms:	Pelargonium vein clearing
Euonymus vulgaris	(?) cytorhabdovirus
Common names:	Pelargonium zonate spot
European spindletree;	ourmiavirus
Spindletree	Pepino mosaic potexvirus
Susceptible to:	Pepper Indian mottle
Arabis mosaic nepovirus	potyvirus
Strawberry latent ringspot (?) nepovirus	Pepper mild mosaic (?) potyvirus
Euonymus japonica	Pepper mild mottle
Susceptible to:	tobamovirus
Euonymus fasciation (?) rhabdovirus	Pepper Moroccan tombusvirus
Euonymus (?) rhabdovirus	Pepper mottle potyvirus
Beta vulgaris	Pepper ringspot tobravirus
Common names:	Pepper severe mosaic
Beet	potyvirus
Susceptible to:	Pepper Texas bigeminivirus
Alfalfa mosaic alfamovirus	Pepper veinal mottle
Arabis mosaic nepovirus	potyvirus
Arracacha A nepovirus	Physalis mosaic tymovirus
Asparagus 2 ilarvirus	Pittosporum vein yellowing
Asparagus 3 potexvirus	nucleorhabdovirus
Barley stripe mosaic hordeivirus	Plantain X potexvirus
Beet 1 alphacryptovirus	Plum American line pattern ilarvirus
Beet 2 alphacryptovirus	Plum pox potyvirus
Beet 3 alphacryptovirus	Poinsettia mosaic (?) tymovirus
Beet curly top hybrigeminivirus	Poplar mosaic carlavirus
Beet distortion mosaic virus	Potato 14R (?) tobamovirus
Beet leaf curl (?) rhabdovirus	Potato A potyvirus
Beet mild yellowing luteovirus	Potato Andean mottle comovirus
Beet mosaic potyvirus	Potato aucuba mosaic potexvirus
Beet necrotic yellow vein furovirus	Potato black ringspot nepovirus
Beet pseudo-yellows (?) closterovirus	Potato mop-top furovirus
Beet soil-borne furovirus	Potato T trichovirus
Beet western yellows luteovirus	Potato U nepovirus
Beet yellow net (?) luteovirus	Potato V potyvirus
Beet yellow stunt closterovirus	Potato X potexvirus
Beet yellows closterovirus	Potato Y potyvirus
Broad bean wilt fabavirus	Potato yellow dwarf nucleorhabdovirus
Butterbur mosaic (?) carlavirus	Primula mosaic potyvirus
	Primula mottle (?) potyvirus
	Prune dwarf ilarvirus
	Radish mosaic comovirus
	Raspberry ringspot

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Cacao necrosis nepovirus	nepovirus
Cacao yellow mosaic tymovirus	Red clover necrotic mosaic dianthovirus
Cactus X potexvirus	Red clover vein mosaic carlavirus
Caraway latent (?) nepovirus	Rhynchosia mosaic bigeminivirus
Carnation latent carlavirus	Ribgrass mosaic tobamovirus
Carnation mottle carmovirus	Rose (?) tobamovirus
Carnation vein mottle potyvirus	Rubus Chinese seed-borne (?) nepovirus
Celery latent (?) potyvirus	Silene X (?) potexvirus
Cherry leaf roll nepovirus	Solanum nodiflorum mottle sobemovirus
Chickpea chlorotic dwarf (?) monogeminivirus	Sonchus cytorhabdovirus
Chicory yellow blotch (?) carlavirus	Sowbane mosaic sobemovirus
Clover yellow mosaic potexvirus	Soybean crinkle leaf (?) bigeminivirus
Clover yellow vein potyvirus	Soybean mild mosaic virus
Cowpea chlorotic mottle bromovirus	Soybean mosaic potyvirus
Cowpea mild mottle (?) carlavirus	Spinach latent ilarvirus
Croton yellow vein mosaic bigeminivirus	Strawberry latent ringspot (?) nepovirus
Cucumber mosaic cucumovirus	Sunn-hemp mosaic tobamovirus
Cucumber soil-borne carmovirus	Sweet clover necrotic mosaic dianthovirus
Cycas necrotic stunt nepovirus	Sweet potato latent (?) potyvirus
Cymbidium ringspot tombusvirus	Sweet potato mild mottle ipomovirus
Dogwood mosaic (?) nepovirus	Sweet potato ringspot (?) nepovirus
Elderberry carlavirus	Tamarillo mosaic potyvirus
Elderberry latent (?) carmovirus	Telfairia mosaic potyvirus
Elm mottle ilarvirus	Tobacco etch potyvirus
Epirus cherry ourmiavirus	Tobacco leaf curl bigeminivirus
Foxtail mosaic potexvirus	Tobacco mild green mosaic tobamovirus
Grapevine Bulgarian latent nepovirus	Tobacco mosaic satellivirus
Grapevine fanleaf nepovirus	Tobacco mosaic tobamovirus
Groundnut eyespot potyvirus	Tobacco mottle umbravirus
Helenium S carlavirus	Tobacco necrosis necrovirus
Heracleum latent trichovirus	Tobacco necrosis satellivirus
Humulus japonicus ilarvirus	Tobacco necrotic dwarf luteovirus
Impatiens latent (?) potexvirus	Tobacco rattle tobravirus
Lettuce infectious yellows (?) closterovirus	Tobacco ringspot nepovirus
Lettuce mosaic potyvirus	Tobacco streak ilarvirus
Lettuce speckles mottle umbravirus	Tobacco stunt varicosavirus
Lilac chlorotic leafspot capillovirus	Tobacco vein-distorting (?) luteovirus
Marigold mottle potyvirus	Tobacco vein mottling potyvirus
Mulberry latent carlavirus	Tobacco wilt potyvirus
Odontoglossum ringspot tobamovirus	Tobacco yellow dwarf monogeminivirus
Parsnip leafcurl virus	Tobacco yellow net (?) luteovirus
Parsnip yellow fleck sequivirus	Tobacco yellow vein assistor (?) luteovirus
Pea seed-borne mosaic potyvirus	Tobacco yellow vein (?) umbravirus
Peanut clump furovirus	Tomato aspermy cucumovirus
Peanut stunt cucumovirus	Tomato Australian leafcurl bigeminivirus
Pelargonium line pattern (?) carmovirus	Tomato black ring nepovirus
Pepper ringspot tobravirus	

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Physalis mild chlorosis (?) luteovirus	Tomato bushy stunt tombusvirus
Potato 14R (?) tobamovirus	Tomato golden mosaic bigeminivirus
Potato black ringspot nepovirus	Tomato mild mottle (?) potyvirus
Potato M carlavirus	Tomato mosaic tobamovirus
Potato mop-top furovirus	Tomato mottle bigeminivirus
Potato T trichovirus	Tomato Peru potyvirus
Potato U nepovirus	Tomato ringspot nepovirus
Radish mosaic comovirus	Tomato spotted wilt tospovirus
Raspberry ringspot nepovirus	Tomato top necrosis (?) nepovirus
Red clover necrotic mosaic dianthovirus	Tomato yellow leaf curl bigeminivirus
Ribgrass mosaic tobamovirus	Tomato yellow mosaic bigeminivirus
Rubus Chinese seed-borne (?) nepovirus	Tulare apple mosaic ilarvirus
Sowbane mosaic sobemovirus	Tulip chlorotic blotch potyvirus
Soybean dwarf luteovirus	Tulip halo necrosis (?) virus
Spinach latent ilarvirus	Turnip mosaic potyvirus
Strawberry latent ringspot (?) nepovirus	Turnip rosette sobemovirus
Subterranean clover red leaf luteovirus	Ullucus mild mottle tobamovirus
Sunn-hemp mosaic tobamovirus	Ullucus mosaic potyvirus
Sweet potato mild mottle ipomovirus	Watermelon mosaic 2 potyvirus
Tobacco etch potyvirus	Wild potato mosaic potyvirus
Tobacco mosaic tobamovirus	Wisteria vein mosaic potyvirus
Tobacco necrosis necrovirus	*Petunia* x *hybrida*
Tobacco rattle tobravirus	Common names:
Tobacco ringspot nepovirus	Common garden petunia;
Tobacco streak ilarvirus	Garden petunia
Tobacco stunt varicosavirus	Susceptible to:
Tobacco yellow dwarf monogeminivirus	Abelia latent tymovirus
Tomato black ring nepovirus	Alfalfa mosaic alfamovirus
Tulip halo necrosis (?) virus	Alstroemeria (?) ilarvirus
Tulip X potexvirus	Alstroemeria mosaic potyvirus
Turnip mosaic potyvirus	Amaranthus leaf mottle potyvirus
Viola mottle potexvirus	Amaranthus mosaic (?) potyvirus
Spinacia oleracea	Aquilegia (?) potyvirus
Common names:	Arabis mosaic nepovirus
Spinach	Arracacha A nepovirus
Susceptible to:	Arracacha B (?) nepovirus
Alfalfa mosaic alfamovirus	Artichoke latent potyvirus
Amaranthus leaf mottle potyvirus	Artichoke vein banding (?) nepovirus
Arabis mosaic nepovirus	Artichoke yellow ringspot nepovirus
Asparagus 3 potexvirus	Asparagus 2 ilarvirus
Barley stripe mosaic hordeivirus	Bean yellow mosaic potyvirus
Bean yellow mosaic potyvirus	Beet curly top hybrigeminivirus
Beet curly top hybrigeminivirus	Beet leaf curl (?) rhabdovirus
Beet leaf curl (?) rhabdovirus	Beet mild yellowing luteovirus
Beet mild yellowing luteovirus	Beet mosaic potyvirus
Beet mosaic potyvirus	Beet necrotic yellow vein furovirus
Beet necrotic yellow vein furovirus	Beet pseudo-yellows (?) closterovirus
Beet pseudo-yellows (?) closterovirus	Beet soil-borne furovirus
Beet soil-borne furovirus	Beet western yellows luteovirus
Beet western yellows luteovirus	Beet yellows closterovirus
Beet yellows closterovirus	Black raspberry necrosis virus
Black raspberry necrosis virus	Broad bean V (?) potyvirus
Broad bean wilt fabavirus	Butterbur mosaic (?) carlavirus
Canavalia maritima mosaic (?) potyvirus	Cacao necrosis nepovirus
Carnation mottle carmovirus	Caper latent carlavirus
Carnation ringspot dianthovirus	Carnation mottle carmovirus
Carnation vein mottle potyvirus	Cassava green mottle nepovirus
Celery latent (?) potyvirus	Cassava Indian mosaic bigeminivirus
Cherry leaf roll nepovirus	Cassava Ivorian bacilliform ourmiavirus
Clover yellow mosaic potexvirus	Celery latent (?) potyvirus
Clover yellow vein potyvirus	Cherry leaf roll nepovirus
Cowpea mild mottle (?) Carlavirus	Chicory yellow mottle nepovirus
Cowpea mosaic comovirus	Chrysanthemum B carlavirus
Croton yellow vein mosaic bigeminivirus	Citrus ringspot virus
Cucumber leaf spot carmovirus	Cowpea chlorotic mottle bromovirus
Cucumber mosaic cucumovirus	Cowpea mosaic comovirus
Cycas necrotic stunt nepovirus	Cowpea severe mosaic comovirus
Cymbidium ringspot tombusvirus	Croton yellow vein mosaic bigeminivirus
Dandelion yellow mosaic sequivirus	Cucumber leaf spot carmovirus
Daphne Y potyvirus	Cymbidium ringspot tombusvirus
Dogwood mosaic (?) nepovirus	Datura distortion mosaic potyvirus
Elderberry latent (?) carmovirus	Datura innoxia Hungarian mosaic (?) potyvirus
Elm mottle ilarvirus	Datura mosaic (?) potyvirus
Epirus cherry ourmiavirus	Dogwood mosaic (?) nepovirus
Foxtail mosaic potexvirus	Eggplant green mosaic potyvirus
Galinsoga mosaic carmovirus	Eggplant mosaic tymovirus
Habenaria mosaic (?) potyvirus	Eggplant mottled dwarf nucleorhabdovirus
Heracleum latent trichovirus	Elderberry latent (?) carmovirus
Lettuce infectious yellows (?) closterovirus	Elm mottle ilarvirus
Lettuce mosaic potyvirus	Epirus cherry ourmiavirus
Lettuce necrotic yellows cytorhabdovirus	Galinsoga mosaic carmovirus
Lettuce speckles mottle umbravirus	Grapevine chrome mosaic nepovirus
Lucerne Australian latent nepovirus	Grapevine fanleaf nepovirus
Lucerne Australian symptomless (?) nepovirus	Groundnut eyespot potyvirus
Lucerne transient streak sobemovirus	Guar top necrosis virus
Lychnis ringspot hordeivirus	Henbane mosaic potyvirus
Melon Ourmia ourmiavirus	Hibiscus latent ringspot nepovirus
Melothria mottle (?) potyvirus	Hibiscus yellow mosaic (?) tobamovirus
Milk vetch dwarf nanavirus	Hippeastrum mosaic potyvirus
Mulberry latent carlavirus	Honeysuckle latent carlavirus
Nandina mosaic (?) potexvirus	Humulus japonicus ilarvirus
Nicotiana velutina mosaic (?) furovirus	Kyuri green mottle mosaic tobamovirus
Oat blue dwarf marafivirus	Lamium mild mottle fabavirus
Okra mosaic tymovirus	Lettuce infectious yellows (?) closterovirus
Parietaria mottle ilarvirus	Lettuce necrotic yellows cytorhabdovirus
Parsnip leafcurl virus	Lilac chlorotic leafspot capillovirus
Parsnip mosaic potyvirus	Lilac mottle carlavirus
	Lisianthus necrosis (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Parsnip yellow fleck sequivirus	necrovirus
Patchouli mosaic potyvirus	Lucerne Australian symptomless (?) nepovirus
Pea early browning tobravirus	Lucerne transient streak sobemovirus
Pea streak carlavirus	Lychnis ringspot hordeivirus
Peanut chlorotic streak caulimovirus	Marigold mottle potyvirus
Peanut clump furovirus	Melandrium yellow fleck bromovirus
Peanut mottle potyvirus	Melilotus mosaic (?) potyvirus
Peanut stunt cucumovirus	Melon Ourmia ourmiavirus
Pelargonium flower break carmovirus	Narcissus mosaic potexvirus
Pelagonium line pattern (?) carmovirus	Neckar River tombusvirus
Pepper Moroccan tombusvirus	Olive latent ringspot nepovirus
Pepper ringspot tobravirus	Olive latent 2 (?) ourmiavirus
Petunia asteroid mosaic tombusvirus	Paprika mild mottle tobamovirus
Physalis mild chlorosis (?) luteovirus	Parietaria mottle ilarvirus
Potato 14R (?) tobamovirus	Parsnip yellow fleck sequivirus
Potato T trichovirus	Passionfruit Sri Lankan mottle (?) potyvirus
Potato U nepovirus	Passionfruit woodiness potyvirus
Radish mosaic comovirus	Pea early browning tobravirus
Raspberry ringspot neprovirus	Pea seed-borne mosaic potyvirus
Red clover necrotic mosaic dianthovirus	Peach enation (?) nepovirus
Ribgrass mosaic tubamovirus	Peanut chlorotic streak caulimovirus
Rose (?) tobamovirus	Peanut clump furovirus
Sowbane mosaic sobemovirus	Peanut green mosaic potyvirus
Soybean mild mosaic virus	Peanut stunt cucumovirus
Spinach latent ilarvirus	Peanut yellow spot tospovirus
Spinach temperate alphacryptovirus	Pelargonium line pattern (?) carmovirus
Statice Y potyvirus	Pelargonium vein clearing (?) cytorhabdovirus
Strawberry latent ringspot (?) nepovirus	Pepper mild mottle tobamovirus
Sunflower ringspot (?) ilarvirus	Pepper Moroccan tombusvirus
Sunn-hemp mosaic tobamovirus	Pepper ringspot tobravirus
Sweet potato mild mottle ipomovirus	Pepper severe mosaic potyvirus
Tobacco necrosis necrovirus	Pepper veinal mottle potyvirus
Tobacco necrotic dwarf luteovirus	Petunia asteroid mosaic tombusvirus
Tobacco rattle tobravirus	Petunia vein clearing (?) caulimovirus
Tobacco ringspot nepovirus	Physalis mosaic tymovirus
Tobacco streak ilarvirus	Pittosporum vein yellowing nucleorhabdovirus
Tobacco stunt varicosavirus	Plantago mottle tymovirus
Tomato black ring nepovirus	Plantain X potexvirus
Tomato bushy stunt tombusvirus	Plum American line pattern ilarvirus
Tomato spotted wilt tospovirus	Plum pox potyvirus
Tulip halo necrosis (?) virus	Poplar mosaic carlavirus
Tulip X potexvirus	Potato 14R (?) tobamovirus
Turnip mosaic potyvirus	Potato Andean latent tymovirus
Vallota mosaic potyvirus	Potato aucuba mosaic potexvirus
Viola mottle potexvirus	Potato black ringspot nepovirus
Watermelon mosaic 2 potyvirus	Potato mop-top furovirus
Wineberry latent virus	Potato U nepovirus
Wisteria vein mosaic potyvirus	Potato yellow mosaic bigeminivirus
Cleome spinosa	Primula mosaic potyvirus
Synonyms:	Prune dwarf ilarvirus
Cleome hassleriana; *Cleome*	Prunus necrotic ringspot ilarvirus

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
arborea; *Cleome pungens*	Raspberry ringspot nepovirus
Common names:	Ribgrass mosaic tobamovirus
Spider-flower	Rose (?) tobamovirus
Susceptible to:	Rubus Chinese seed-borne (?) nepovirus
Turnip yellow mosaic tymovirus	Solanum nodiflorum mottle sobemovirus
Gloriosa rothschildiana	Sonchus cytorhabdovirus
Synonyms:	Soybean crinkle leaf (?) bigeminivirus
Gloriosa superba; *Gloriosa abyssinica*; *Gloriosa homblei*; *Gloriosa hybrid*; *Gloriosa simplex*; *Gloriosa speciosa*; *Gloriosa virescens*	Soybean mild mosaic virus
	Soybean mosaic potyvirus
	Spinach latent ilarvirus
Common names:	Sunflower ringspot (?) ilarvirus
Flame lily; Glory lily; Climbing lily; Creeping lily	Sunn-hemp mosaic tobamovirus
Susceptible to:	Sweet potato mild mottle ipomovirus
Gloriosa fleck (?) nucleorhabdovirus	Tamarillo mosaic potyvirus
Tradescantia zebrina	Tobacco etch potyvirus
Synonyms:	Tobacco leaf curl bigeminivirus
Tradescantia pendula; *Zebrina pendula*	Tobacco mild green mosaic tobamovirus
Common names:	Tobacco rattle tobravirus
Wandering-jew	Tobacco ringspot nepovirus
Susceptible to:	Tobacco streak ilarvirus
Tradescantia-Zebrina potyvirus	Tobacco stunt varicosavirus
Chrysanthemum morifolium	Tobacco yellow vein (?) umbravirus
Synonyms:	Tomato black ring nepovirus
Dendranthema x *grandiflorum*; *Anthemis grandiflorum*; *Anthemis stipulacea*; *Chrysanthemum sinense*; *Chrysanthemum stipulaceum;* *Dendranthema* x *morifolium; Matricaria morifolia*	Tomato bushy stunt tombusvirus
	Tomato golden mosaic bigeminivirus
	Tomato infectious chlorosis (?) closterovirus
Common names:	Tomato mosaic tobamovirus
Florist's chrysanthemum; Mum; Chrisanthemum	Tomato mottle bigeminivirus
Susceptible to:	Tomato Peru potyvirus
Chrysanthemum B carlavirus	Tomato ringspot nepovirus
Cucumber mosaic cucumovirus	Tomato spotted wilt tospovirus
Oat blue dwarf marafivirus	Tomato top necrosis (?) nepovirus
Tomato aspermy cucumovirus	Tomato vein clearing nucleorhabdovirus
Helianthus annuus	Tomato yellow mosaic bigeminivirus
Synonyms:	Tulip chlorotic blotch potyvirus
Helianthus annuus var. *macrocarpus*; *Helianthus lenticularis*	Tulip halo necrosis (?) virus
	Turnip mosaic potyvirus
Common names:	Ullucus mild mottle tobamovirus
Common annual sunflower; Sunflower; Hopi sunflower; Common sunflower; Girasol	Ullucus mosaic potyvirus
	White clover mosaic potexvirus
Susceptible to:	Wisteria vein mosaic potyvirus
Alfalfa mosaic alfamovirus	
Artichoke curly dwarf (?) potexvirus	
Artichoke latent potyvirus	
Beet western yellows luteovirus	
Bidens mosaic potyvirus	
Bidens mottle potyvirus	
Cassia mild mosaic (?) carlavirus	
Cherry leaf roll nepovirus	
Citrus ringspot virus	
Clover yellow mosaic potexvirus	
Clover yellow vein	*Theobroma cacao*

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
potyvirus	Synonyms:
Cucumber mosaic	*Theobroma sativa*
cucumovirus	Common names:
Cymbidium ringspot	Cacao; Chocolate-tree
tombusvirus	Susceptible to:
Elm mottle ilarvirus	Cacao necrosis nepovirus
Galinsoga mosaic	Cacao swollen shoot
carmovirus	badnavirus
Humulus japonicus ilarvirus	Cacao yellow mosaic
Lettuce infectious yellows	tymovirus
(?) closterovirus	Cowpea mild mottle (?)
Maracuja mosaic (?)	carlavirus
tobamovirus	Okra mosaic tymovirus
Melandrium yellow fleck	*Tetragonia tetragonioides*
bromovirus	Susceptible to:
Patchouli mosaic potyvirus	Abelia latent tymovirus
Peanut stunt cucumovirus	Alfalfa mosaic alfamovirus
Pepper veinal mottle	Alstroemeria (?) ilarvirus
potyvirus	Alstroemeria mosaic
Physalis mosaic tymovirus	potyvirus
Prune dwarf ilarvirus	Alstroemeria streak (?)
Prunus necrotic ringspot	potyvirus
ilarvirus	Amaranthus leaf mottle
Red clover necrotic mosaic	potyvirus
dianthovirus	Apple stem pitting virus
Sunflower crinkle (?)	Arabis mosaic nepovirus
umbravirus	Arracacha A nepovirus
Sunflower mosaic (?)	Arracacha B (?) nepovirus
potyvirus	Arracacha latent (?)
Sunflower ringspot (?)	carlavirus
ilarvirus	Arracacha Y potyvirus
Sunflower yellow blotch (?)	Asparagus 1 potyvirus
umbravirus	Asparagus 3 potexvirus
Tobacco necrosis necrovirus	Asystasia gangetica mottle
Tobacco rattle tobravirus	(?) potyvirus
Tobacco streak ilarvirus	Bean common mosaic
Tomato black ring	potyvirus
nepovirus	Bean yellow mosaic
Tomato spotted wilt	potyvirus
tospovirus	Beet leaf curl (?)
Tropaeolum 2 potyvirus	rhabdovirus
Convolvulus arvensis	Beet mild yellowing
Common names:	luteovirus
Field bindweed	Beet mosaic potyvirus
Insusceptible to:	Beet necrotic yellow vein
Carnation vein mottle	furovirus
potyvirus	Beet western yellows
Cornus florida	luteovirus
Common names:	Beet yellows closterovirus
Flowering dogwood;	Broad bean necrosis
American-boxwood	furovirus
Susceptible to:	Cacao necrosis nepovirus
Cherry leaf roll nepovirus	Cacao yellow mosaic
Dogwood mosaic (?)	tymovirus
nepovirus	Carnation mottle
Synonyms:	carmovirus
Corylus avellana f. *aurea*;	Carnation ringspot
Corylus avellana f. *contorta*;	dianthovirus
Corylus avellana f. *fusco-rubra*;	Carnation vein mottle
Corylus avellana f. *heterophylla*;	potyvirus
Corylus avellana f.	Cassava green mottle
pendula; *Corylus avellana*	nepovirus
var. *aurea*; *Corylus avellana* var.	Cassava Ivorian bacilliform
contorta; *Corylus avellana* var.	ourmiavirus
fusco-rubra; *Corylus avellana* var.	Cassia mild mosaic (?)
heterophylla;	carlavirus
Corylus avellana var.	Celery latent (?) potyvirus
pendula; *Corylus heterophylla*	Chickpea distortion mosaic
Common names:	potyvirus
European filbert; European	Chrysanthemum B
hazel; Avellana; Hazelnut	carlavirus
Susceptible to:	Clover wound tumor
Tulare apple mosaic	phytoreovirus
ilarvirus	Clover yellow vein

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Kalanchoe blossfeldiana	potyvirus
Synonyms:	Commelina X potexvirus
Kalanchoe globulifera var.	Cowpea mild mottle (?)
coccinea	carlavirus
Susceptible to:	Cucumber mosaic
Kalanchoe latent carlavirus	cucumovirus
Kalanchoe mosaic (?)	Cycas necrotic stunt
potyvirus	nepovirus
Kalanchoe top-spotting	Cymbidium ringspot
badnavirus	tombusvirus
Brassica napus var. *napus*	Dasheen mosaic potyvirus
Synonyms:	Dioscorea latent (?)
Brassica campestris f.	potexvirus
annua; *Brassica campestris* f.	Dogwood mosaic (?)
biennis; *Brassica napus* f. *annua*;	nepovirus
Brassica napus f. *biennis*; *Brassica*	Eucharis mottle (?)
napus ssp. *oleifera;*	nepovirus
Brassica napus var. *annua;*	Foxtail mosaic potexvirus
Brassica napus var. *biennis;*	Groundnut eyespot
Brassica napus var. *oleifera*	potyvirus
Common names:	Habenaria mosaic (?)
Rape; Colza; Bird rape;	potyvirus
Canola	Helenium S carlavirus
Susceptible to:	Heracleum latent trichovirus
Watercress yellow spot	Hibiscus latent ringspot
virus	nepovirus
Brassica nigra	Hypochoeris mosaic (?)
Synonyms:	furovirus
Brassica nigra var.	Impatiens latent (?)
abyssinica; *Sinapis nigra*	potexvirus
Common names:	Iris mild mosaic potyvirus
Black mustard	Kalanchoe isometric virus
Susceptible to:	Kalanchoe latent carlavirus
Beet western yellows	Lamium mild mottle
luteovirus	fabavirus
Ribgrass mosaic	Lettuce big-vein
tobamovirus	varicosavirus
Turnip mosaic potyvirus	Lettuce mosaic potyvirus
Turnip yellow mosaic	Lilac chlorotic leafspot
tymovirus	capillovirus
Citrullus vulgaris	Lily X potexvirus
Synonyms:	Lisianthus necrosis (?)
Citrullus lanatus var.	necrovirus
lanatus; *Citrullus aedulis*; *Citrullus*	Lucerne Australian latent
lanatus var. *caffer*; *Colocynthis*	nepovirus
citrullus; *Cucurbita citrullus*	Lychnis ringspot
Common names:	hordeivirus
Watermelon	Maclura mosaic
Susceptible to:	macluravirus
Cucumber green mottle	Malva veinal necrosis (?)
mosaic tobamovirus	potexvirus
Cucumber vein yellowing	Marigold mottle potyvirus
virus	Melandrium yellow fleck
Telfairia mosaic potyvirus	bromovirus
Watermelon chlorotic stunt	Melilotus mosaic (?)
bigeminivirus	potyvirus
Wild cucumber mosaic	Melon Ourmia ourmiavirus
tymovirus	Narcissus latent
Cucurbita maxima	macluravirus
Common names:	Narcissus mosaic potexvirus
Squash; Pumpkin	Narcissus tip necrosis (?)
Susceptible to:	carmovirus
Apple mosaic ilarvirus	Nerine potyvirus
Bean yellow mosaic	Nerine X potexvirus
potyvirus	Odontoglossum ringspot
Beet curly top	tobamovirus
hybrigeminivirus	Okra mosaic tymovirus
Cherry leaf roll nepovirus	Ornithogalum mosaic
Clover yellow mosaic	potyvirus
potexvirus	Parietaria mottle ilarvirus
Cucumber leaf spot	Parsnip leafcurl virus
carmovirus	Parsnip yellow fleck
Cucumber mosaic	sequivirus
cucumovirus	Patchouli mottle (?)

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Daphne X potexvirus	potyvirus
Elm mottle ilarvirus	Pea early browning
Eucharis mottle (?)	tobravirus
nepovirus	Pea mosaic potyvirus
Grapevine fanleaf nepovirus	Pea seed-borne mosaic potyvirus
Humulus japonicus ilarvirus	Peach enation (?) nepovirus
Kyuri green mottle mosaic	Peanut clump furovirus
tobamovirus	Peanut green mosaic
Lettuce infectious yellows	potyvirus
(?) closterovirus	Peanut stunt cucumovirus
Lisianthus necrosis (?)	Pelargonium flower break
necrovirus	carmovirus
Maracuja mosaic (?)	Pelargonium line pattern (?)
tobamovirus	carmovirus
Melandrium yellow fleck	Pepino mosaic potexvirus
bromovirus	Pepper ringspot tobravirus
Melon leaf curl	Plantago mottle tymovirus
bigeminivirus	Poplar mosaic carlavirus
Melothria mottle (?)	Potato 14R (?) tobamovirus
potyvirus	Potato black ringspot
Papaya ringspot potyvirus	nepovirus
Pea seed-borne mosaic	Potato mop-top furovirus
potyvirus	Potato U nepovirus
Peanut stunt cucumovirus	Primula mosaic potyvirus
Poplar mosaic carlavirus	Red clover necrotic mosaic
Prune dwarf ilarvirus	dianthovirus
Prunus necrotic ringspot	Ribgrass mosaic
ilarvirus	tobamovirus
Radish mosaic comovirus	Solanum nodiflorum mottle
Sowbane mosaic	sobemovirus
sobemovirus	Soybean dwarf luteovirus
Squash leaf curl	Spinach latent ilarvirus
bigeminivirus	Strawberry latent ringspot
Squash mosaic comovirus	(?) nepovirus
Strawberry latent ringspot	Sweet clover necrotic
(?) nepovirus	mosaic dianthovirus
Sunflower ringspot (?)	Sweet potato mild mottle
ilarvirus	ipomovirus
Tobacco necrosis necrovirus	Sweet potato ringspot (?)
Tobacco ringspot nepovirus	nepovirus
Tobacco streak ilarvirus	Tamus latent (?) potexvirus
Tomato bushy stunt	Telfairia mosaic potyvirus
tombusvirus	Tobacco etch potyvirus
Watermelon curly mottle	Tobacco necrosis necrovirus
bigeminivirus	Tobacco ringspot nepovirus
Watermelon mosaic 1	Tobacco stunt varicosavirus
potyvirus	Tomato black ring
Watermelon mosaic 2	nepovirus
potyvirus	Tomato bushy stunt
Wild cucumber mosaic	tombusvirus
tymovirus	Tomato vein clearing
Zucchini yellow fleck	nucleorhabdovirus
potyvirus	Tulip chlorotic blotch
Zucchini yellow mosaic	potyvirus
potyvirus	Tulip halo necrosis (?) virus
Cycas revoluta	Tulip X potexvirus
Common names:	Turnip crinkle carmovirus
Sago cycas; Sotesu-nut	Turnip mosaic potyvirus
Susceptible to:	Ullucus C comovirus
Cycas necrotic stunt	Ullucus mild mottle
nepovirus	tobamovirus
Dioscorea alata	Ullucus mosaic potyvirus
Synonyms:	Vallota mosaic potyvirus
Dioscorea rubella	Viola mottle potexvirus
Common names:	Watermelon mosaic 2
Yam; Greater yam; Water	potyvirus
yam; Winged yam; White yam;	Wineberry latent virus
Guyana arrowroot; Ten-months	Wisteria vein mosaic
yam; Name-de-Agna	potyvirus
Susceptible to:	*Camellia japonica*
Dioscorea alata potyvirus	Synonyms:
Dioscorea trifida (?)	*Camellia japonica* var.
potyvirus	*hortensis*; *Camellia japonica* var.
Yam internal brown spot (?)	*hozanensis*; *Camellia japonica* var.

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
badnavirus	*spontanea*; *Thea japonica*
Yam mosaic potyvirus	Common names:
Vaccinium corymbosum	Common camellia
Synonyms:	Susceptible to:
Vaccinium constablaei	Camellia yellow mottle (?)
Common names:	varicosavirus
Highbush blueberry;	*Thunbergia alata*
Blueberry; American blueberry;	Common names:
Swamp blueberry	Black-eyed-Susan-vine;
Susceptible to:	Ojitos-negros
Blueberry leaf mottle	Susceptible to:
nepovirus	Datura yellow vein
Blueberry necrotic shock	nucleorhabdovirus
ilarvirus	Prune dwarf ilarvirus
Blueberry red ringspot	*Daphne cneorum*
caulimovirus	Common names:
Blueberry scorch carlavirus	Rose daphne; Garland
Blueberry shoestring	flower
sobemovirus	Susceptible to:
Croton bonplandianus	Daphne S (?) carlavirus
Synonyms:	Daphne X potexvirus
Croton sparsiflorus	Daphne Y potyvirus
Susceptible to:	*Corchorus olitorius*
Croton yellow vein mosaic	Common names:
bigeminivirus	Nalta jute; Tossa jute; Tussa
Euphorbia marginata	jute
Synonyms:	Susceptible to:
Euphorbia variegata	Okra mosaic tymovirus
Common names:	*Tropaeolum majus*
Snow-on-the-mountain	Common names:
Susceptible to:	Garden nasturtium; Indian-
Beet curly top	cress; Mastuerzo
hybrigeminivirus	Susceptible to:
Dulcamara mottle	Alfalfa mosaic alfamovirus
tymovirus	Apple mosaic ilarvirus
Poinsettia mosaic (?)	Arabis mosaic nepovirus
tymovirus	Beet curly top
Watermelon mosaic 2	hybrigeminivirus
potyvirus	Beet western yellows
Quercus velutina	luteovirus
Common names:	Broad bean wilt fabavirus
Black oak	Cherry leaf roll nepovirus
Susceptible to:	Clover mild mosaic virus
Oak ringspot virus	Cucumber mosaic
Eustoma russellianum	cucumovirus
Synonyms:	Cymbidium mosaic
Bilamista grandiflora;	potexvirus
Eustoma grandiflorum;	Cymbidium ringspot
Lisianthius russellianus	tombusvirus
Common names:	Lamium mild mottle
Bluebells; Prairie-gentian	fabavirus
Susceptible to:	Lettuce infectious yellows
Bean yellow mosaic	(?) closterovirus
potyvirus	Melandrium yellow fleck
Lisianthus necrosis (?)	bromovirus
necrovirus	Nasturtium mosaic (?)
Pelargonium peltatum	potyvirus
Synonyms:	Okra mosaic tymovirus
Geranium peltatum	Pea early browning
Common names:	tobravirus
Ivy geranium; Hanging	Poplar mosaic carlavirus
geranium	Red clover necrotic mosaic
Susceptible to:	dianthovirus
Pelargonium flower break	Ribgrass mosaic
carmovirus	tobamovirus
Pelargonium line pattern (?)	Strawberry latent ringspot
carmovirus	(?) nepovirus
Pelargonium vein clearing	Sunn-hemp mosaic
(?) cytorhabdovirus	tobamovirus
Pelargonium x domesticum	Tobacco rattle tobravirus
Insusceptible to:	Tobacco ringspot nepovirus
Aster chlorotic stunt (?)	Tomato black ring
carlavirus	nepovirus
Carnation vein mottle	Tomato spotted wilt

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
potyvirus	tospovirus
Chrysanthemum B	Tropaeolum 2 potyvirus
carlavirus	White clover mosaic
Saintpaulia ionantha	potexvirus
Common names:	*Anethum graveolens*
African violet; Usambara	Synonyms:
violet	*Anethum sowa;*
Susceptible to:	*Peucedanum graveolens*
Carnation ringspot	Common names:
dianthovirus	Dill; Dill seed; Garden dill;
Saintpaulia leaf necrosis (?)	Eneldo; Aneto; Fenouil-batard;
rhabdovirus	Endro
Ribes nigrum	Susceptible to:
Common names:	Artichoke yellow ringspot
Black currant; Cassis	nepovirus
Susceptible to:	Carrot mottle umbravirus
Strawberry latent ringspot (?)	Carrot red leaf luteovirus
nepovirus	Celery mosaic potyvirus
Hypericum perforatum	Heracleum latent trichovirus
Common names:	Parsnip yellow fleck
Common St. John's-wort;	sequivirus
Klamathweed; St. John's-wort;	*Foeniculum vulgare*
Goatweed	Common names:
Insusceptible to:	Fennel; Florence fennel;
Carnation ringspot	Finocchio; Hinojo
dianthovirus	Susceptible to:
Hyacinthus orientalis	Coriander feathery red vein
Common names:	nucleorhabdovirus
Common hyacinth	Insusceptible to:
Susceptible to:	Celery yellow spot (?)
Hyacinth mosaic potyvirus	luteovirus
Crocus vernus	Heracleum latent trichovirus
Susceptible to:	Parsnip yellow fleck
Iris severe mosaic potyvirus	sequivirus
Freesia refracta	*Valeriana officinalis*
Synonyms:	Common names:
Freesia leichtlinii; *Gladiolus refractus*	Common valeriana; Garden-heliotrope
Susceptible to:	Susceptible to:
Freesia leaf necrosis	Watermelon mosaic 2
varicosavirus	potyvirus
Freesia mosaic potyvirus	*Verbena hybrida*
Gladiolus	Common names:
Susceptible to:	Garden verbena; Florist's
Artichoke Italian latent	verbena
nepovirus	Susceptible to:
Bean yellow mosaic	Carnation ringspot
potyvirus	dianthovirus
Cycas necrotic stunt	Melilotus mosaic (?)
nepovirus	potyvirus
Narcissus latent	*Viola odorata*
macluravirus	Common names:
Iris	English violet; Sweet violet;
Susceptible to:	Garden violet
Iris mild mosaic potyvirus	Susceptible to:
Iris severe mosaic potyvirus	Tulip X potexvirus
Juglans regia	Viola mottle potexvirus
Synonyms:	*Vitis vinifera*
Juglans duclouxiana;	Common names:
Juglans fallax; *Juglans kamaonica*;	European grape; Wine
Juglans orientis; *Juglans regia* ssp.	grape; Vid
kamaonica; *Juglans regia* var.	Susceptible to:
orientis; *Juglans*	Arabis mosaic nepovirus
regia var. *sinensis*; *Juglans*	Artichoke Italian latent
sinensis	nepovirus
Common names:	Grapevine A (?) trichovirus
English walnut; Persian	Grapevine ajinashika
walnut; Nogal	disease (?) luteovirus
susceptible to:	Grapevine Algerian latent
Cherry leaf roll nepovirus	tombusvirus
Leguminosae	Grapevine B (?) trichovirus
Insusceptible to:	Grapevine Bulgarian latent
Voandzeia necrotic mosaic	nepovirus
tymovirus	Grapevine chrome mosaic

TABLE 4-continued

Plant or Virus Name	Plant or Virus Name
Mimosa pudica	nepovirus
Common names:	Grapevine corky bark-associated (?) closterovirus
Sensitive-plant; Touch-me-not; Shame plant	Grapevine fanleaf nepovirus
Insusceptible to:	Grapevine fleck virus
Mimosa mosaic virus	Grapevine leafroll-associated (?) closteroviruses
Soybean mosaic potyvirus	Grapevine line pattern (?)
Lilium	ilarvirus
Susceptible to:	Grapevine stem pitting
Lily mottle potyvirus	associated closterovirus
Tomato aspermy	Grapevine stunt virus
cucumovirus	Petunia asteroid mosaic
Tulip breaking potyvirus	tombusvirus
Tulipa	Strawberry latent ringspot
Susceptible to:	(?) nepovirus
Arabis mosaic nepovirus	*Zingiber officinale*
Tobacco rattle tobravirus	Synonyms:
Tomato black ring	*Amomum zingiber*
nepovirus	Common names:
Tomato bushy stunt	Ginger; Jengibre
tombusvirus	Susceptible to:
	Ginger chlorotic fleck (?) sobemovirus

[0126] Overview of Bioinformatics Methods

[0127] A. Phred, Phrap and Consed

[0128] Phred, Phrap and Consed are a set of programs which read DNA sequencer traces, make base calls, assemble the shotgun DNA sequence data and analyze the sequence regions that are likely to contribute to errors. Phred is the initial program used to read the sequencer trace data, call the bases and assign quality values to the bases. Phred uses a Fourier-based method to examine the base traces generated by the sequencer. The output files from Phred are written in FASTA, phd or scf format. Phrap is used to assemble contiguous sequences from only the highest quality portion of the sequence data output by Phred. Phrap is amenable to high-throughput data collection. Finally, Consed is used as a "finishing tool" to assign error probabilities to the sequence data. Detailed description of the Phred, Phrap and Consed software and its use can be found in the following references which are hereby incorporated herein by reference: Ewing, B., Hillier, L., Wendl, M. C. and Green, P. (1998) "Base-calling of automated sequencer traces using Phred. I. Accuracy assessment."*Genome Res.* 8: 175-178; Ewing, B. and Green, P. (1998) "Base-calling of automated sequencer traces using Phred. II. Error probabilities."*Genome Res.* 8:186-194; Gordon, D., Abajian, C. and Green, P. (1998) "Consed: a graphical tool for sequence finishing."*Genome Res.* 8: 195-202.

[0129] B. BLAST

[0130] The BLAST ("Basic Local Alignment Search Tool") set of programs may be used to compare the large numbers of sequences and obtain homologies to known protein families. These homologies provide information regarding the function of newly sequenced genes. Detailed description of the BLAST software and its uses can be found in the following references which are hereby incorporated herein by reference: Altschul, S. F., Gish, W., Miller, W., Myers, E. W. and Lipman, D. J. (1990) "Basic Local Alignment Search Tool."*J. Mol. Biol.* 215: 403-410; Alts-

chul, S. F. (1991) "Amino acid subsitution matrices from an informatics theoretic perspective."*J. Mol. Biol.* 219: 555-565.

[0131] Generally, BLAST performs sequence similarity searching and is divided into 5 basic programs: (1) BLASTP compares an amino acid sequence to a protein sequence database; (2) BLASTN compares a nucleotide sequence to a nucleic acid sequence database; (3) BLASTX compares translated protein sequences done in 6 frames to a protein sequence database; (4) TBLASTN compares a protein sequence to a nucleotide sequence database that is translated into all 6 reading frames; (5) TBLASTX compares the 6 frame translated protein sequence to the 6-frame translation of a nucleotide sequence database. Programs (3)-(5) may be used to identify weak similarities in nucleic acid sequence.

[0132] The BLAST program is based on the High Segment Pair (HSP), two sequence fragments of arbitrary but equal length whose alignment is locally maximized and whose alignment meets or exceeds a cutoff threshold. BLAST determines multiple HSP sets statistically using "sum" statistics. The score of the HSP is then related to its expected chance of frequency of occurrence, E. The value, E, is dependent on several factors such as the scoring system, residue composition of sequences, length of query sequence and total length of database. In the output file will be listed these E values, these are typically in a histogram format, and are useful in determining levels of statistical significance at the user's predefined expectation threshold. Finally, the Smallest Sum Probability, P(N) is the probability of observing the shown matched sequences by chance alone and is typically in the range of 0-1.

[0133] BLAST measures sequence similarity using a matrix of similarity scores for all possible pairs of residues and these specify scores for aligning pairs of amino acids. The matrix of choice for a specific use depends on several factors: the length of the query sequence and whether or not a close or distant relationship between sequences is suspected. Several matrices are available including PAM40, PAM120, PAM250, BLOSUM 62 and BLOSUM 50. Altschul et al. (1990) found PAM120 to be the most broadly sensitive matrix (i.e. point accepted mutation matrix per 100 residues). However, in some cases the PAM120 matrix may not find short but strong or long but weak similarities between sequences. In these cases, pairs of PAM matrices may be used, such as PAM40 and PAM 250, and the results compared. Typically, PAM 40 is used for database searching with a query of 9-21 residues long, while PAM 250 is used for lengths of 47-123.

[0134] The BLOSUM (Blocks Substitution Matrix) series of matrices are constructed based on percent identity between two sequence segments of interest. Thus, the BLOSUM62 matrix is based on a matrix of sequence segments in which the members are less than 62% identical. BLOSUM62 shows very good performance for BLAST searching. However, other BLOSUM matrices, like the PAM matrices, may be useful in other applications. For example, BLOSUM45 is particularly strong in profile searching.

[0135] C. FASTA

[0136] The FASTA suite of programs permits the evaluation of DNA and protein similarity based on local sequence alignment. The FASTA search algorithm utilizes Smith/Waterman- and Needleman/Wunsch-based optimization methods. These algorithms consider all of the alignment possibilities between the query sequence and the library in the highest-scoring sequence regions. The search algorithm proceeds in four basic steps:

[0137] 1). The identities or pairs of identities between the two DNA or protein sequences are determined. The ktup parameter, as set by the user, is operative and determines how many consecutive sequence identities are required to indicate a match.

[0138] 2). The regions identified in step 1 are re-scored using a PAM or BLOSUM matrix. This allows conservative replacements and runs of identities shorter than that specified by ktup to contribute to the similarity score.

[0139] 3). The region with the single best scoring initial region is used to characterize pairwise similarity and these scores are used to rank the library sequences.

[0140] 4). The highest scoring library sequences are aligned using the Smith-Waterman algorithm. This final comparison takes into account the possible alignments of the query and library sequence in the highest scoring region.

[0141] Further detailed description of the FASTA software and its use can be found in the following reference which is hereby incorporated herein by reference: Pearson, W. R. and Lipman, D. J. (1988) "Improved tools for biological sequence comparison."*Proc.Natl.Acad. Sci.* 85: 2444-2448.

[0142] D. Pfam

[0143] Despite the large number of different protein sequences determined through genomics-based approaches, relatively few structural and functional domains are known. Pfam is a computational method that utilizes a collection of multiple alignments and profile hidden Markov models of protein domain families to classify existing and newly found protein sequences into structural families. Detailed description of the Pfam software and its uses can be found in the following references which are hereby incorporated herein by reference: Sonhammer, E. L. L., Eddy, S. R. and Durbin, R. (1997) "Pfam: a comprehensive database of protein domain families based on seed alignments."*Proteins: Structure, Function and Genetics* 28: 405-420; Sonhammer, E. L. L., Eddy, S. R. Bimey, E., Bateman, A. and Durbin, R. (1998) "Pfam: multiple sequence alignments and HMM-profiles of protein domains."*Nucleic Acids Res.* 26: 320-322; Bateman, A., Birney, E., Durbin, R., Eddy, S. R. Finn, R. D. and Sonhammer, E. L. L. (1999) *Nucleic Acids Res.* 27: 260-262.

[0144] Pfam 3.1, the latest version, includes 54% of proteins in SWISS_PROT and SP-TrEMBL-5 as a match to the database and includes expectation values for matches. Pfam consists of parts A and B. Pfam-A, contains a hidden Markov model and includes curated families. Pfam-B, uses the Domainer program to cluster sequence segments not included in Pfam-A. Domainer uses pairwise homology data from Blastp to construct aligned families.

[0145] Alternative protein family databases that may be used include PRINTS and BLOCKS, which both are based on a set of ungapped blocks of aligned residues. However,

these programs typically contain short conserved regions whereas Pfam represents a library of complete domains that facilitates automated annotation. Comparisons of Pfam profiles may also be performed using genomic and EST data with the programs, Genewise and ESTwise, respectively. Both of these programs allow for introns and frameshifting errors.

[0146] E. BLOCKS

[0147] The determination of sequence relationships between unknown sequences and those that have been categorized can be problematic because background noise increases with the number of sequences, especially at a low level of similarity detection. One recent approach to this problem has been tested that efficiently detects and confirms weak or distant relationships among protein sequences based on a database of blocks. The BLOCKS database provides multiple alignments of sequences and contains blocks or protein motifs found in known families of proteins.

[0148] Other programs such as PRINTS and Prodom also provide alignments, however, the BLOCKS database differs in the manner in which the database was constructed. Construction of the BLOCKS database proceeds as follows: one starts with a group of sequences that presumably have one or more motifs in common, such as those from the PROSITE database. The PROTOMAT program then uses a motif finding program to scan sequences for similarity looking for spaced triplets of amino acids. The located blocks are then entered into the MOTOMAT program for block assembly. Weights are computed for all sequences. Following construction of a BLOCKS database one can use BLIMPS to perform searches of the BLOCKS database. Detailed description of the construction and use of a BLOCKS database can be found in the following references which are hereby incorporated herein by reference: Henikoff, S. and Henikoff, J. G. (1994) "Protein family classification based on searching a database of blocks." Genomics 19: 97-10; Henikoff, J. G. and Henikoff, S. (1996) "The BLOCKS database and its applications." Meth. Enz. 266: 88-105.

[0149] F. PRINTS

[0150] The PRINTS database of protein family fingerprints can be used in addition to BLOCKS and PROSITE. These databases are considered to be secondary databases because they diagnose the relationship between sequences that yield function information. Presently, however, it is not recommended that these databases be used alone. Rather, it is strongly suggested that these pattern databases be used in conjunction with each other so that a direct comparison of results can be made to analyze their robustness.

[0151] Generally, these programs utilize pattern recognition to discover motifs within protein sequences. However, PRINTS goes one step further, it takes into account not simply single motifs but several motifs simultaneously that might characterize a family signature. Other programs, such as PROSITE, rely on pattern recognition but are limited by the fact that query sequences must match them exactly. Thus, sequences that vary slightly will be missed. In contrast, the PRINTS database fingerprinting approach is capable of identifying distant relatives due to its reliance on the fact that sequences do not have match the query exactly. Instead they are scored according to how well they fit each motif in the signature. Another advantage of PRINTS is that it allows the user to search both PRINTS and PROSITE simultaneously. A detailed description of the use of PRINTS can be found in the following references which are hereby incorporated herein by reference:Attwood, T. K., Beck, M. E., Bleasly, A. J., Degtyarenko, K., Michie, A. D. and Parry-Smith, D. J. (1997) *Nucleic Acids Res.* 25: 212-216.

[0152] Related, Variant, Altered and Extended Nucleic Acid Sequences

[0153] In one embodiment, the invention provides a polypeptide comprising the amino acid sequence encoded by a cDNA identified by a polynucleotide sequence chosen from the group consisting of SEQ ID NO: 1-122. The invention also encompasses variant polypeptides which retain the functional activity of causing a dwarf phenotype in a plant. A preferred variant is one having at least 80%, more preferably 90%, and most preferably 95% amino acid sequence identity to the original polypeptide sequence.

[0154] It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding the same polypeptide, some bearing minimal homology to the nucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence, and all such variations are to be considered as being specifically disclosed.

[0155] It may be advantageous to produce nucleotide sequences encoding polypeptide or its derivatives possessing a substantially different codon usage. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding a polypeptide and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

[0156] The invention also encompasses production of DNA sequences having the function of causing a dwarf phenotype in a plant, or portions thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into such a sequence or any portion thereof.

[0157] Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the polynucleotide sequences shown in SEQ ID NO: 1-122, under various conditions of stringency. Hybridization conditions are based on the melting temperature (T_m) of the nucleic acid binding complex or probe, as taught in Wahl, G. M. and S. L. Berger (1987; Methods Enzymol. 152:399-407) and Kimmel, A. R. (1987; Methods Enzymol. 152:507-511), and may be used at a defined stringency.

[0158] Altered nucleic acid sequences causing a dwarf phenotype in a plant which are encompassed by the invention include deletions, insertions, or substitutions of different nucleotides resulting in a polynucleotide that is functionally equivalent. The encoded polypeptide may also contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and consequently remains functionally equivalent. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the functional activity is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid; positively charged amino acids may include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; phenylalanine and tyrosine.

[0159] Also included within the scope of the present invention are alleles of the genes encoded by cDNAs identified by the polynucleotide sequences SEQ ID NO: 1-122. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

[0160] Methods for DNA sequencing which are well known and generally available in the art may be used to practice any embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE® (US Biochemical Corporation, Cleveland, Ohio), TAQ® polymerase (U.S. Biochemical Corporation, Cleveland, Ohio), thermostable T7 polymerase (Amersham Pharmacia Biotech, Chicago, Ill.), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE® amplification system (Life Technologies, Rockville, Md.). Preferably, the process is automated with machines such as the MICROLAB® 2200 (Hamilton Company, Reno, Nev.), PTC200 DNA Engine thermal cycler (MJ Research, Watertown, Mass.) and the ABI 377™ DNA sequencer (Perkin Elmer).

[0161] The nucleic acid sequences of the invention may be extended utilizing a partial nucleotide sequence and employing various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, one method which may be employed, "restriction-site" PCR, uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). In particular, genomic DNA is first amplified in the presence of primer to linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

[0162] Inverse PCR may also be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). The primers may be designed using OLIGO 4.06 primer analysis software (National Biosciences Inc., Plymouth, Minn.), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72° C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

[0163] Another method which may be used is capture PCR which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119). In this method, multiple restriction enzyme digestions and ligations may also be used to place an engineered double-stranded sequence into an unknown portion of the DNA molecule before performing PCR.

[0164] Another method which may be used to retrieve unknown sequences is that of Parker, J. D. et al. (1991; Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER™ DNA Walking Kits libraries (Clontech, Palo Alto, Calif.) to walk in genomic DNA. This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

[0165] When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Also, random-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into the 5' and 3' non-transcribed regulatory regions.

[0166] Capillary electrophoresis systems which are commercially available (e.g. from PE Biosystems, Inc., Foster City, Calif.) may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled devise camera. Output/light intensity may be converted to electrical signal using appropriate software (e.g. GENOTYPER® and SEQUENCE NAVIGATOR® from PE Biosystems, Foster City, Calif.) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

[0167] Vectors, Engineering, and Expression of Sequences

[0168] In another embodiment of the invention, cDNA sequences or fragments thereof which have the function of causing a dwarf phenotype in a plant, or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of polypeptides in appropriate host cells.

Due to the inherent degeneracy of the genetic code, other polynucleotide sequences which encode substantially the same or a functionally equivalent polypeptide also may be produced and these sequences may be used to clone and express the polypeptide of interest.

[0169] As will be understood by those of skill in the art, it may be advantageous to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

[0170] The polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter their polypeptide encoding sequences for a variety of reasons, including but not limited to, introducing alterations which modify the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

[0171] In another embodiment of the invention, natural, modified, or recombinant polynucleotide sequences having the function of causing a dwarf phenotype in a plant may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of the dwarf phenotype, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the wild-type coding sequence and the heterologous protein sequence, so that the wild-type polypeptide may be cleaved and purified away from the heterologous moiety.

[0172] In another embodiment, polynucleotide sequences having the function of causing a dwarf phenotype in a plant may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232). Alternatively, the polypeptide product may be produced using chemical methods to synthesize the amino acid sequence. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) Science 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A™ peptide synthesizer (PE Corporation, Norwalk, Conn.).

[0173] The newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (see, e.g., Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; or Creighton, supra). Additionally, the amino acid sequence, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

[0174] In order to express a biologically active polypeptide, the encoding nucleotide sequences or their functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence.

[0175] Methods which are well known to those skilled in the art may be used to construct expression vectors containing nucleic acid sequences and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York, N.Y, both of which are hereby incorporated by reference herein.

[0176] A variety of expression vector/host systems may be utilized to contain and express sequences having the function of causing a dwarf phenotype in a plant. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV; brome mosaic virus) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

[0177] The "control elements" or "regulatory sequences" are those non-translated regions of the vector—enhancers, promoters, 5' and 3' translated regions—which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the BLUESCRIPT® phagemid (Stratagene, La Jolla, Calif.) or PSPORT1™ plasmid (Life Technologies, Inc., Rockville, Md.) and the like may be used. The baculovirus polyhedrin promoter may be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO; and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) may be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of the sequence, vectors based on SV40 or EBV may be used with an appropriate selectable marker.

[0178] In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the resulting gene product. For example, when large quantities of gene product are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifinctional *E.coli* cloning and expression vectors such as BLUESCRIPT® phagemid (Stratagene, La Jolla, Calif.), in which a sequence may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β-ga-

lactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEMX™ vectors (Promega Corporation, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

[0179] In the yeast, *Saccharomyces cerevisiae,* a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) Methods Enzymol. 153:516-544.

[0180] In cases where plant expression vectors are used, the expression of sequences having the function of causing a dwarf phenotype in a plant may be driven by any of a number of promoters. In a preferred embodiment, plant vectors are created using a recombinant plant virus containing a recombinant plant viral nucleic acid, as described in PCT publication WO 96/40867 which is hereby incorporated herein by reference. Subsequently, the recombinant plant viral nucleic acid which contains one or more non-native nucleic acid sequences may be transcribed or expressed in the infected tissues of the plant host and the product of the coding sequences may be recovered from the plant, as described in WO 99/36516, which is hereby incorporated herein by reference.

[0181] An important feature of this embodiment is the use of recombinant plant viral nucleic acids which contain one or more non-native subgenomic promoters capable of transcribing or expressing adjacent nucleic acid sequences in the plant host and which result in replication and local and/or systemic spread in a compatible plant host. The recombinant plant viral nucleic acids have substantial sequence homology to plant viral nucleotide sequences and may be derived from an RNA, DNA, cDNA or a chemically synthesized RNA or DNA. A partial listing of suitable viruses is described below.

[0182] The first step in producing recombinant plant viral nucleic acids according to this particular embodiment is to modify the nucleotide sequences of the plant viral nucleotide sequence by known conventional techniques such that one or more non-native subgenomic promoters are inserted into the plant viral nucleic acid without destroying the biological function of the plant viral nucleic acid. The native coat protein coding sequence may be deleted in some embodiments, placed under the control of a non-native subgenomic promoter in other embodiments, or retained in a further embodiment. If it is deleted or otherwise inactivated, a non-native coat protein gene is inserted under control of one of the non-native subgenomic promoters, or optionally under control of the native coat protein gene subgenomic promoter. The non-native coat protein is capable of encapsidating the recombinant plant viral nucleic acid to produce a recombinant plant virus. Thus, the recombinant plant viral nucleic acid contains a coat protein coding sequence, which may be native or a nonnative coat protein coding sequence, under control of one of the native or non-native subgenomic promoters. The coat protein is involved in the systemic infection of the plant host.

[0183] Some of the viruses which meet this requirement include viruses from the tobamovirus group such as Tobacco Mosaic virus (TMV), Ribgrass Mosaic Virus (RGM), Cowpea Mosaic virus (CMV), Alfalfa Mosaic virus (AMV), Cucumber Green Mottle Mosaic virus watermelon strain (CGMMV-W) and Oat Mosaic virus (OMV) and viruses from the brome mosaic virus group such as Brome Mosaic virus (BMV), broad bean mottle virus and cowpea chlorotic mottle virus. Additional suitable viruses include Rice Necrosis virus (RNV), and geminiviruses such as tomato golden mosaic virus (TGMV), Cassava latent virus (CLV) and maize streak virus (MSV). However, the invention should not be construed as limited to using these particular viruses, but rather the method of the present invention is contemplated to include all plant viruses at a minimum.

[0184] Other embodiments of plant vectors used for the expression of sequences having the function of stunting a plant include, for example, viral promoters such as the 35S and 19S promoters of CaMVused alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196.

[0185] An insect system may be used to express the polypeptides of the invention. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in Trichoplusia larvae. The sequences encoding the gene product may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or Trichoplusia larvae in which the gene product may be expressed (Engelhard, E. K. et al. (1994) Proc. Nat. Acad. Sci. 91:3224-3227).

[0186] In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the nucleic acid sequences of the invention may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the relevant gene product in infected host cells (Logan, J. and Shenk, T. (1984) Proc. Natl. Acad. Sci. 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

[0187] Specific initiation signals may also be used to achieve more efficient translation of the nucleic acid sequences of the invention. Such signals include the ATG initiation codon and adjacent sequences. In cases where a sequence, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162).

[0188] In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

[0189] For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express a specific gene product may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

[0190] Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) Cell 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1980) Cell 22:817-23) genes which can be employed in tk^- or $aprt^-$ cells, respectively. Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection; for example, dhfr, which confers resistance to methotrexate (Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-70); npt, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. et al (1981) J. Mol. Biol. 150: 1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, supra). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-51). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, β-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) Methods Mol. Biol. 55:121-131).

[0191] Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if a nucleic acid sequence of the invention is inserted within a marker gene sequence, recombinant cells containing that specific sequence can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence of the invention under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

[0192] Alternatively, host cells which contain a nucleic acid sequence of the invention and which express its gene product may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

[0193] The presence of polynucleotide sequences of the invention can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or portions or fragments of polynucleotide sequence of interest. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the sequences of interest to detect transformants containing the relevant DNA or RNA. As used herein "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of at least about 10 nucleotides and as many as about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20-25 nucleotides, which can be used as a probe or amplimer.

[0194] A variety of protocols for detecting and measuring the expression of a cDNA, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on the protein is preferred, but a competitive binding assay may be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; J. Exp. Med. 158:1211-1216).

[0195] A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to the polynucleotide sequences of the invention include oligonucleotide labeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof

may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits from Pharmacia & Upjohn (Kalamazoo, Mich.), Promega Corporation (Madison, Wis.) and U.S. Biochemical Corp. (Cleveland, Ohio). Suitable reporter molecules or labels, which may be used, include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

[0196] Host cells transformed with a polynucleotide sequence of the invention may be cultured under conditions suitable for the expression and recovery of protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of its corresponding polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join polynucleotide sequences of the invention to a nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS™ extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (available from Invitrogen, San Diego, Calif.) between the purification domain and polypeptide of interest may be used to facilitate purification. One such expression vector provides for expression of a fusion protein comprising a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, Prot. Exp. Purif 3: 263-281,) while the enterokinase cleavage site provides a means for purifying polypeptide of interest from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; DNA Cell Biol. 12:441-453).

[0197] In addition to recombinant production, a fragment of a polypeptide of the invention may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) J. Am. Chem. Soc. 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using the Applied Biosystems 431A peptide synthesizer (Perkin Elmer). Various peptide fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

[0198] In additional embodiments, the nucleotide and amino acid sequences of the present invention may be incorporated into any molecular biology techniques yet to be developed, provided these new techniques rely on properties of nucleotide and amino acid sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

[0199] The following examples further illustrate the present invention. These examples are intended merely to be illustrative of the present invention and are not to be construed as being limiting. The examples are intended specifically to illustrate the various methods used to identify and characterize the cDNAs of the present invention and the method by which they can be used to cause a dwarf phenotype in a plant.

EXAMPLES

[0200] I. Construction and Characterization of a Normalized Arabidopsis cDNA library in GENEWARE® Vectors

[0201] A. Plant Tissue Generation:

[0202] *Arabidopsis thaliana* ecotype Columbia (0) seeds were sown and grown on PEAT LITE MIX (Speedling Inc., Sun City, Fla.) supplemented with NUTRICOTE fertilizer (Plantco Inc., Ontario, Canada). Plants were grown under a 16-hour light/8-hour dark cycle in an environmental controlled growth chamber. The temperature was set at 22° C. for daytime and 18° C. for nighttime. The entire plant, root, leaves and all aerial parts were collected 4 weeks post sowing. Tissue was washed in deionized water and frozen in liquid nitrogen.

[0203] B. RNA Extraction:

[0204] High quality total RNA is isolated using a hot borate method. All solutions were made in DEPC-treated, double-deionized water and autoclaved. All glassware, mortars, pestles, spatulas, and glass rods were baked at 400° C. for four hours. All plasticware was DEPC-treated for at least three hours and then autoclaved.

[0205] Thirty-five milliliters of XT buffer (0.2 M Na borate decahydrate, 30 mM EGTA, 1% SDS (w/v), 1% deoxycholate, sodium) per 10 grams of tissue was dispensed into 50 milliliter Falcon tubes. PVP-40, 000 was added to a final concentration of 2% (w/v). NP-40 was added to a final concentration of 1% (w/v). Tubes were placed in an 80° C. water bath. The mortar and pestles were then pre-cooled in liquid nitrogen. Proteinase K (0.5 mg/ml XT buffer) was dispensed into 250 ml centrifuge bottles and the bottles were then placed on ice.

[0206] The tissue was added to the pre-chilled mortar and pestle and ground to a fine powder. Working as quickly as possible, the tissue was transferred to a glass beaker using a spatula chilled in liquid nitrogen. DTT (1.54 mg/ml XT buffer) was added to the XT buffer/PVP/NP-40 buffer and was immediately added to the ground tissue. The tissue was homogenized using a polytron at level 5 for one minute. The homogenate was decanted into the 250 ml centrifuge bottle containing the proteinase K. The homogenate was incubated at 42° C., 100 rpm for 1.5 hours. Eighty microliters of 2M KCl/ml of XT buffer was added to the homogenate and gently swirled until mixed. The samples were then incubated on ice for one hour. The samples were centrifuged at 12,000× G in a BECKAN® JA-14 rotor (Beckman Instruments, Inc., Fullerton, Calif.) for 20 minutes at 4° C. to remove debris. The supernatant was then filtered through a funnel lined with sterile miracloth into a sterile 250 ml

centrifuge bottle. Eight molar LiCl was added to a final concentration of 2M LiCl and the samples were incubated on ice overnight.

[0207] Precipitated RNA was pelleted by centrifugation at 12,000× G in a BECKMAN® JA-14 rotor for 20 minutes (Beckman Instruments, Inc., Fullerton, Calif.) and the supernatant was discarded. The RNA pellet was washed in 5 milliliters of cold 2M LiCl in 30 ml centrifuge tubes. Glass rods and gentle vortexing were used to break and disperse the RNA pellet. The pellets were centrifuged in a Beckman JA-20 rotor for 10 krpm at 4° C. for 10 minutes. The supernatant was decanted. This wash step was repeated 3 times until the supernatant was relatively colorless. The RNA pellet was resuspended in 5 milliliters of 10 Tris-Cl (pH 7.5). The insoluble material was pelleted in a JA-17 at 10 k rpm for 10 minutes at 4° C. The supernatant was transferred to another 30 ml centrifuge tube and 0.1× volume of 2M K-acetate (pH 5.5) was added. The samples were incubated on ice for 15 minutes and centrifuged in a BECKMAN® JA-17 rotor (Beckman Instruments, Inc., Fullerton, Calif.) at 10 k rpm, 4° C., for 10 minutes to remove polysaccharides and insoluble material. The supernatant was transferred to a sterile 30 ml centrifuge tube and RNA was precipitated by adding 2.5× volumes of 100% ethanol. The RNA was precipitated overnight at −20° C. The precipitated RNA was pelleted by centrifugation at 9 krpm, 4° C. for 30 minutes in a JA-17 rotor. The RNA pellet was washed with 5 milliliters of cold 70% ethanol and centrifuged in a JA-17 rotor at 9 k rpm, 4° C. for 10 minutes. The residual ethanol was removed using a BECKMAN® speed vac (Beckman Instruments, Inc., Fullerton, Calif.). The RNA pellet was resuspended in 3 milliliters of DEPC-ddH_2O+1 mM EDTA. The RNA was precipitated with 0.1× volumes of 3M Na-acetate pH 6.0 and 2× volumes of cold 100% ethanol. The RNA was put at -80° C. for storage. A BECKMAN® spectrophotometer (Beckman Instruments, Inc., Fullerton, Calif.) was used to measure absorbance (A) at A_{260} and A_{280}. The A_{260} was used to determine concentration (40 μg RNA/ml=1 A_{260} absorbance unit) and the A_{260}/A_{280} ratio was used to determine the initial quality of the RNA (1.8 to 2.0 is good).

[0208] The yield of total RNA from 60 g of tissue is ~15 mg. Then, mRNA was isolated from total RNA using oligo $(dT)_{25}$ DYNABEADS® (Dynal, Inc., Lake Success, N.Y.). Typically, 1% of total RNA population can be recovered as mRNA in *Arabidopsis thaliana* whole plant and from 5 μg of poly A^+ RNA, approximate 4.5 μg of single strand cDNA and 6.7 μg of double strand cDNA was synthesized.

[0209] C. cDNA Synthesis:

[0210] Poly A^+ RNA was purified from total RNA using the oligo $(dT)_{25}$ DYNABEADS® kit (Dynal, Inc., Lake Success, N.Y.) according to manufacturer's instructions. Briefly, DYNABEADS® was resuspended by mixing on a roller and transfer 600 μl to an RNase free tube. The beads were further equilibriated with 2× binding buffer (20 mM Tris-HCl, pH 7.5, 1M LiCl, 2 mM EDTA) twice and resuspended in 200 μl of 2× binding buffer. Total RNA 1 mg (200 μl) was heated at 70° C. for 5 minutes and incubated with the above oligo $(dT)_{25}$ DYNABEADS® for 10 min at RT. The supernatant containing unbound rRNA and tRNA was subsequently removed by magnetic stand and washed twice with 1× wash buffer (10 mM Tris-HCl, pH 7.5, 0.15M LiCl, 1 mM EDTA). The mRNA was eluted from the DYNABEADS® in ddH_2O and used as the starting material for double strand cDNA synthesis.

[0211] Double strand cDNA was synthesized either with NotI-$(dT)_{25}$ primer or on oligo $(dT)_{25}$ DYNABEADS® based on the manufacturer's instruction (Gibco-BRL superscript system). Typically, 5 μg of poly A^+ RNA was annealed and reverse transcribed at 37° C. with SUPERSCRIPT II reverse transcriptase (Stratagene, La Jolla, Calif.). For the non-normalized cDNA library, double stranded cDNAs were ligated to a 500 to 1000-fold molar excess SalI adaptor, restriction enzyme NotI digested and size-selected by column fractionation. Those cDNAs were then cloned directionally into the XhoI-NotI sites of the TMV expression vector, 1057 N/P.

[0212] D. Normalization Procedure:

[0213] For the normalized cDNA preparation, the supernatant was removed from the DYNABEADS® and the cDNA containing beads were washed twice with 1× TE buffer. To carry out the normalization process, the second strand cDNA were eluted from the beads. 100 μl of TE buffer was added to the beads and heated at 95° C. for 5 min and the supernatant was then collected on magnetic stand. The above procedure was repeated once to ensure complete elution. The yield of second strand cDNA was quantitated using a UV spectrophotometer.

[0214] First strand cDNA beads is combined with second strand cDNA in 4× SSC, 5× Denhardt's and 0.5% SDS for multiple rounds of short hybridization. Since the second strand cDNA was synthesized using the first strand cDNA as the template, approximately the same amount of first and second strand cDNAs were present in the hybridization reaction. Nine μg of second strand cDNA in 200 μl of 1× TE buffer was added to the cDNA driver (first strand cDNA on beads) in a screw cap tube. The reaction was heated at 95° C. for 5 min, then 60 μl of 20× SSC, 30 μl of 50× Denhardt's (1% of Ficoll, 1% of polyvinylpyrrolidone and 1% of bovine serum albumin) and 15μl of 10% SDS were added and the reaction was brought to 65° C. for 8 hours.

[0215] The beads and supernatant were separated at 65° C. by magnet. The supernatant was transferred to a fresh tube and kept at 65° C. The beads were regenerated by adding 200 μl of ddH_2O and heated at 95° C. for 5 min. We collected the beads for the next round of hybridization and kept the solution containing the bound second strand cDNA for further analysis. The partially normalized second strand cDNA solution was added back to the regenerated beads and a return to another round of hybridization of 8 hours. This procedure was repeated 4-5 times.

[0216] E. Slot Blot Analysis:

[0217] To follow the process of cDNA normalization a rapid slot blot procedure was developed. Following sequencing of 960 cDNAs, 46 cDNAs were selected to follow the representation of various classes of cDNAs through the normalization procedure. Based on their frequency of appearance in the sequence, these clones represent transcripts of different expression levels (high, moderate and low). Ten nanograms of each cDNA were deposited onto a HYBOND™-N^+ membrane (Amersham Pharmacia Biotech, Chicago, Ill.) along with control vector (pBS) and water controls. DNA was denatured, neutralized, and sub-

sequently crosslinked into the membrane using UV-STRATALINKER™ 2400 (Stratagene, La Jolla, Calif.).

[0218] cDNAs from either the non-normalized or normalized pool were labelled with ^{32}P and hybridized on the slot blot membrane overnight at 65° C. in 1% bovine serum albumin, 1 mM ethylenediaminetetraacetic acid (EDTA), 0.5 M sodium phosphate (pH 7.2), and 7% sodium dodecyl sulfate (SDS). Then, blots were washed once in 1× SSC/0.2% SDS for 20 min at room temperature followed by two washes in 0.2× SSC/0.2% SDS for 20 min. at 65° C. The resulting membranes were then developed using a PHOSPHORIMAGER™ (Amersham Pharmacia Biotech, Chicago, Ill.) and quantitated using available software.

[0219] F. Conversion of Single-Stranded Normalized cDNAs to Double-Stranded Form:

[0220] Second strand normalized cDNA in hybridization solution was purified by QIAQUICK™ column (QIAGEN GmbH, Hilden, Germany) and eluted in 88 μl of ddH_2O (total 1.2 μg of DNA is recovered). One μl (3 μg) of NotI-oligo dT primer was added and heated at 95° C. for 5 min followed by cool down to 37° C. The first strand cDNA was extended with T7 DNA polymerase (Amersham Pharmacia Biotech, Chicago, Ill.) in the presence of dNTP in 120 μl reaction at 37° C. for 1 hour. T4 DNA polymerase (NEB) was then used to polish the ends following the extension reaction for 5 min at 16° C. The resulting double strand cDNA was ethanol precipitated and ligated with 500- to 1 000-fold molar excess of SalI adaptor followed by NotI digestion. The resulting cDNAs were size-fractionated using a Clontech spin column 400 and the first two fractions that contained the cDNAs were pooled and used for the subsequent cloning process.

[0221] G. Construction of cDNA Libraries in GENEWARE® Vectors:

[0222] (+) Sense cDNA clones were prepared as follows. The Tobacco Mosaic Virus expression vector, 1 056GTN-AT9 was linearized with NotI and XhoI and a 900 bp stuffer DNA was removed. The presence of the stuffer DNA in between those two sites is to ensure the complete digestion by restriction enzymes and thus achieve the high cloning efficiency. The digested vector was gel purified and then used to set up ligation reaction with normalized cDNA SalI-NotI fragments to generate (+) sense cDNA clones.

[0223] (−) Sense cDNA clones were prepared as follows. The Tobacco Mosaic Virus expression vector 1057 NP also linearized with NotI and XhoI and a stuffer DNA fragment was removed. The digested vector was gel purified and used to set up ligation reaction to generate (−) sense strand library.

[0224] Each ligation was transformed into chemically competent *E. coli* cells, DH5 α according to manufacturer's instruction (Life Technologies, Rockville, Md.). Preliminary analysis of cloning efficiency was measured by plating of a small portion of the transformation, while archiving the majority for future applications. Vector-only ligations gave ~2×10^4 cfu/μg vector and ligations with cDNA insertions gave ~5×10^5 cfu/μg.

[0225] H. Analysis of Normalized cDNA Populations:

[0226] With each successive round of kinetic re-association, the total cDNA population is depleted thereby confirming the removal of a population of the cDNA from the mixture at each step. To further understand the consequences of this depletion and measure the relative normalization in cDNA representation following various stages of the kinetic re-association method, slot blots of 46 genes of varying representations were hybridized with probes made from non-normalized and normalized cDNA preparations. The resulting blots were then analyzed for representation by PHOSPHORIMAGER® analysis. The hybridization pattern of non-normalized cDNA to the gene array reveals a quite asymmetric representation with some genes hybridizing with great intensity while others showing no hybridization at all. The variance among hybridization intensities for each spot within the filter was measured by standard deviation and found to be 649. In order to analyze the cDNA fraction depleted from the mixture, the first strand magnetic bead matrix was eluted, a radioactive probe was generated and hybridized to a replica of the slot blot described above. The resulting hybridization intensities indicated that primarily those cDNAs of higher copy number were bound and removed from the normalized cDNA population, confirming that the depletion phenomenon correlated with removal of primarily high copy number cDNAs. The cDNA population not bound to first strand magnetic beads after 5 serial passages was collected, radioactive probe was generated and hybridized to a replica slot blot of known gene set described above. The resulting hybridization pattern (i.e. the relative intensity of the slots on the blot) was in striking contrast to that of the non-normalized cDNA and to that of the bound cDNA fraction. Assuming that the majority of the hybridization signal to the slot blot for the non-normalized cDNA blot results from hybridization to high abundance genes, an initial comparison can be made between the number of bound counts on the normalized versus non-normalized slot blots. This comparison is possible since each probe added to the blots was derived from the same quantity of cDNA material and an equal number of probe counts were applied to the blots. The non-normalized blot contained 17,898 counts while the normalized blot contained only 1494 counts. This represents a 12-fold reduction in overall signal indicating a significant reduction in high gene copy number in the normalized cDNA population.

[0227] When the hybridization intensity of the non-normalized cDNA probe to each gene is plotted against the relative number of counts (following subtraction of the pBS vector control intensity from each sample), there is almost a 4-log difference in sequence representation in the cDNA population and an overall variance in standard deviation of 649-fold. In contrast, the hybridization of normalized cDNA probe to each gene revealed an average of only 32-fold difference. This represents both a reduction in high copy cDNAs and an increased representation in low copy cDNAs by >3 logs. The variance between the most highly represented cDNA and lowest represented cDNA within the normalized cDNA population was ~1.5 logs. The above values characterizing the degree of library normalization are equivalent to those achieved by Soares, et al. (1994).

[0228] I. Analysis of GENEWARE® Clones:

[0229] To ascertain the cloning efficiency of normalized cDNA into each vector and the average insert size, 96 random colonies were picked and grown by standard methods. DNA was isolated from bacteria using a BIOROBOT™ 9600 (QIAGEN GmbH, Hilden, Germany). DNA was digested with Not I and BsiWI restriction endonucleases

(recognition sites flank the cDNA insertion). The digestions were separated on agarose gels and visualized by ethidium bromide staining. The digestions revealed a vector religation background of ~4%. Ligations giving >75% insertions were passed as to quality control and more colonies were picked. Approximently 600 independent clones were analyzed by restriction digestion as described above. Interestingly, a similar percentage of vector background was detected ~4% and the average insert size in the vector was ~1 kb, with many inserts with 2 kb or greater sized inserts. Following analysis of DNA by restriction mapping, DNA was subjected to sequencing and further analysis.

[0230] J. Sequence Analysis of the Normalized Arabidopisis Library in GENEWARE®:

[0231] Initial analysis of non-normalized Arabidopsis cDNA library required the sequencing of 1709 independent clones. Three 96-well plates of randomly picked normalized Arabidopsis library in GENEWARE®[(−) sense] were initially sequenced by primer TP6 to yield 262 5' sequences and passed sequence quality control. Initially, internal cluster analysis was performed to identify identical sequences in this sequence subset. Analysis using BLASTN algorithm showed that of the 262 sequences analyzed, 252 were unique and only 10 were found to cluster into five two-member clusters. We then identified the redundancy of the sequences against the larger public databases. For cluster analysis, we used a very low BLASTX score criteria ($e=10^{-6}$) and compared all sequences against the GENBANK® nr database (United States Department of Health and Human Services). In this manner, we could derive the most information concerning the redundancy, gene type found and open reading frame status of all clones simultaneously. The low BLASTX score was used to allow all possible protein homologues to be identified. The clustering analysis revealed that of the 262 sequences there were 252 single member sequence clusters and five two-gene clusters. This represents 96% singletons from this sample size. The genes appearing more than once in the library varied from two different chlorophyll a/b binding proteins, lipid transport proteins to ferrodoxin-thioredoxin reductases. This result compares quite favorably to the 4 redundant clones (of one gene type) identified by Soares, et al. (1994) from 187 randomly picked clones from one normalized library.

[0232] Further analysis of the sequences from the GENEWARE® normalized cDNA library revealed that of the 262 sequences subjected to BLASTX search of the GENBANK® nr database, 29% of the sequences failed to show significant homology to any characterized protein or open reading frame (ORF). Of the 252 singletons in the library, 179 showed single hit to an identified ORF, while 73 showed no hit. These results suggest that, in spite of the well characterized nature of the sequence database quality libraries can still contain a high proportion of new expressed sequences.

[0233] The excellent representation and extremely low redundancy observed in these initial plates of normalized Arabidopsis cDNAs in GENEWARE® prompted us to sequence additional clones. This was important because there is often a significant bias in small sample sizes with regard to representation. A total of 1,151 sequences passed sequence quality control. Internal cluster analysis showed that ~260 multi-sequence clusters were present, with the highest representation at 6 members and the majority with only 2 members (~150). About 600 unique clusters were identified from the total of 856 clusters from the 1151 sequences. Therefore, from the 1151 sequences analyzed, 1,010 unique genes were identified, or a 87.7% gene discovery rate. In contrast, internal cluster analysis of the non-normalized Arabidopsis cDNA sequences revealed ~840 multi-gene clusters with the highest represented cluster containing 27 members. Cluster analysis of the 1709 non-normalized Arabidopsis cDNAs revealed clusters of 27 members and many other highly populated clusters, a dramatic difference from the normalized cDNAs.

[0234] Further comparison of 1,151 randomly chosen non-normalized sequences for redundancy with the results from the 1,151 normalized population clearly indicated the positive effects of normalization and the greater number of unique genes identified from this normalized population. Many genes that have representations of >12 in the non-normalized library have been reduced to 1-4 members in the normalized population. One chlorophyll a/b binding protein gene exhibited a reduction from 15 members in the non-normalized population to 1 in the normalized library, whereas a gene encoding a distinct chlorophyll a/b binding protein showed less reduction in the normalized gene population. This observation is consistent with the conclusion that certain genes do not undergo the same degree of normalization compared with other genes.

[0235] Additional sequences from the normalized Arabidopsis library were obtained by sequence analysis. BLASTN analysis of the 1,343 normalized sequences revealed that 858 were represented in the Arabidopsis EST database, while the remaining 485 sequences were apparently unique, with no obvious homologue in the database. Of those sequences showing BLASTN hits, 43.6% showed coverage of the first through tenth base in the longest EST in the database. Furthermore, 242 of the 858 (28%) showed 5' sequences that were at the first base of the longest EST or longer. These data show that the cDNAs cloned into GENEWARE® are of significant quality and represent, in many cases, the longest 5' sequences obtained to date. To further ascertain the proportion of cDNAs containing full-length protein open reading frames, we employed the ORF finder program used to analyze the ABRC library for sense clones. This algorithm checks for ATG sequences in the first 70 bases of a sequence and then scans for sequences lacking an in-frame stop codon for at least 300 nt downstream in the same frame. To understand the number of quality ORFs in a library, we used the ABRC library as a benchmark. Analysis of 11,957 sequences within the ABRC library with the ORF finder program revealed 3,207 hits (26.8%) with putative open reading frames. From the 1,343 sequences of the normalized Arabidopsis cDNA library in GENEWARE®, 907 (67.5%) were hits using the ORF finder program. Coupling the number of cDNAs that represent near the 5' end of the known RNA sequence (43.6%) with the number of clones that contain putative intact ORFs (67.5%) testifies to the quality and integrity of the cDNAs in the GENEWARE® vector. These data clearly indicate a high proportion of full-length clones.

[0236] K. Quantity of Normalized Arabidopsis cDNAs Cloned into GENEWARE® Vectors:

[0237] As previously described, the normalized Arabidopsis cDNA population was cloned into GENEWARE® vec-

tors in both the positive (+) and negative (−) sense direction to allow for both overexpression and gene knockout analysis. The total number of clones in the 1057 PN vector in negative orientation was 20,160. These were arrayed into 210 96-well glycerol stock plates. Likewise, 20,160 clones from the ligation of normalized Arabidopsis cDNA in sense orientation into 1056 GTN vector have been arrayed in 210 96-well glycerol stock plates. These numbers clearly show that the GENEWARE® vectors can be used as primary cloning vectors and that very complex libraries can be obtained in two orientations from a single pool on non-amplified normalized cDNA.

[0238] II. Construction of Tissue-Specific *N. benthamiana* cDNA Libraries

[0239] A. mRNA Isolation:

[0240] Leaf, root, flower, meristem, and pathogen-challenged leaf cDNA libraries were constructed. Total RNA samples from 10-5 μg of the above tissues were isolated by TRIZOL reagent (Life Technologies, Rockville, Md.). The typical yield of total RNA was 1 mg. PolyA+RNA was purified from total RNA by DYNABEADS® oligo $(T)_{25}$. Purified mRNA was quantified by UV absorbance at OD_{260}. The typical yield of mRNA was 2% of total RNA. The purity was also determined by the ratio of OD_{260}/OD_{280}. The integrity of the samples has OD values of 1.8-2.0.

[0241] B. cDNA Synthesis:

[0242] cDNA was synthesized from mRNA using the SUPERSCRIPT® plasmid system (Life Technologies, Rockville, Md.) with cloning sites of NotI at the 3' end and SalI at the 5' end. After fractionation through a gel column to eliminate adapter fragments and short sequences, cDNA was cloned into both GENEWARE® vector p1057 NP and phagemid vector PSPORT™ in the multiple cloning region between NotI and XhoI sites. Over 20,000 recombinants were obtained for all of the tissue-specific libraries.

[0243] C. Library Analysis:

[0244] The quality of the libraries was evaluated by checking the insert size and percentage from representative 24 clones. Overall, the average insert size was above 1 kb, and the recombinant percentage was >95%.

[0245] III. Construction of Normalized *N. benthamiana* cDNA Library in GENEWARE® Vectors

[0246] A. cDNA Synthesis.

[0247] A pooled RNA source from the tissues described above was used to construct a normalized cDNA library. Total RNA samples were pooled in equal amounts first, then polyA+RNA was isolated by DYNABEADS® oligo (dT)25. The first strand cDNA was synthesized by the Smart III system (Clontech, Palo Alto, Calif.). During the synthesis, adapter sequences with Sfi1a and Sfi1b sites were introduced by the polyA priming at the 3' end, and 5' end by the template switch mechanism (Clontech, Palo Alto, Calif.). Eight μg first strand cDNA was synthesized from 24 μg mRNA. The yield and size were confirmed by UV absorbance and agarose gel electrophoresis.

[0248] B. Construction of Genomic DNA Driver.

[0249] Genomic DNA driver was constructed by immobilizing biotinylated DNA fragments onto streptavidin-coated magnetic beads. Fifty μg genomic DNA was digested by EcoR1 and BamH1 followed by fill-in reaction using biotin-21-dUTP. The biotinylated fragments were denatured by boiling and immobilized onto DYNABEADS® by the conjugation of streptavidin and biotin.

[0250] C. Normalization Procedure.

[0251] Six μg of the first strand cDNA was hybridized to 1 μg of genomic DNA driver in 100 μl of hybridization buffer (6× SSC, 0.1% SDS, 1× Denhardt's buffer) for 48 hours at 65° C. with constant rotation. After hybridization, the cDNA bound on genomic DNA beads was washed 3 times by 20 μl 1× SSC/0.1% SDS at 65° C. for 15 min and one time by 0.1× SSC at room temperature. The bounded cDNA on the beads was then eluted in 10μl of fresh-made 0.1N NaOH from the beads and purified by using a QIAGEN DNA purification column (QIAGEN GmbH, Hilden, Germany), which yielded 110 ng of normalized cDNA fragments. The normalized first strand cDNA was converted to double strand cDNA in 4 cycles of PCR with Smart primers annealed to the 3' and 5'end adapter sequences.

[0252] D. Evaluation of Normalization Efficiency.

[0253] Ninety-six non-redundant cDNA clones selected from a randomly sequenced pool of 500 clones of a previously constructed whole seedling library were used to construct a nylon array. One hundred ng of the normalized cDNA fragments vs. the non-normalized fragments were radioactively labeled by ^{32}P and hybridized to DNA array nylon filters. Hybridization images and intensity data were acquired by a PHOSPHORIMAGER® (Amersham Pharmacia Biotech, Chicago, Ill.). Since the 96 clones on the nylon arrays represent different abundance classes of genes, the variance of hybridization intensity among these genes on the filter were measured by standard deviation before and after normalization. These results indicated that by using this type of normalization approach, we could achieve a 1 000-fold reduction in variance among this set of genes.

[0254] E. Cloning of Normalized cDNA into GENEWARE® Vector.

[0255] The normalized cDNA fragments were digested by Sfi1 endonuclease, which recognizes 8-bp sites with variable sequences in the middle 4 nucleotides. After size fractionation, the cDNA was ligated into GENEWARE® vector p1057 NP in antisense orientation and transformed into DH5α cells. Over 50,000 recombinants were obtained for this normalized library. The percentage of insert and size were evaluated by Sfi digestion of randomly picked 96 clones followed by electrophoresis on 1% of agarose gel. The average insert size was 1.5 kb, and the percentage of insert was 98% with vector only insertions of >2%.

[0256] F. Sequence Analysis of Normalized cDNA Library.

[0257] As of the date of this report, 2 plates of 96 randomly picked clones have been sequenced from the 5' end of cDNA inserts. One hundred ninety-two quality sequences were obtained after trimming of vector sequences and other standard quality checking and filtering procedure, and subjected to BLASTX search in DNA and protein databases. Over 40% of these sequences had no hit in the databases. Clustering analysis was conducted based on

accession numbers of BLASTX matches among the 112 sequences that had hits in the databases. Only three genes (tumor-related protein, citrin, and rubit) appeared twice. All other members in this group appeared only once. This was a strong indication that this library is well-normalized. Sequence analysis also revealed that 68% of these 192 sequences had putative open reading frames using the ORF finder program (as described above), indicating possible full-length cDNA.

[0258] IV. DNA Preparation

[0259] A. High Throughput Clone Preparation.

[0260] Arraying of the ABRC library into GENEWARE® vectors occurred as previously discussed to obtain ~5,000 antisense and ~3,000 sense clones with minimal redundancy. The ligations were between highly purified and quality controlled GENEWARE® cloning vector plasmids and the corresponding fragments from each individual pool of ABRC clones. Cloning efficiencies were in the range of 1×10^5 to 5×10^5 per μg of plasmid. Colonies were picked using a Flexys Colony Picker (The Sanger Centre, England) and manual methods. Colonies were applied to deep-well cell growth blocks (DWBs) and grown from 18-26 hours at 37° C. at ~500 rpm in the presence of ampicillin concentrations of 500 μg/ml. From the almost 9,000 colonies picked by the Flexys, >97% of the cultures successfully grew. DNA was prepared using the QIAGEN BIOROBOT 9600 DNA robots and QIAGEN 96-well manifolds (manual preparation) at a rate of 2,000 DNA preparations per day. The final throughput, during campaign production, estimated for each system was ~20 plates of 96 samples per day, per production line—robotic or manual. Such throughput could be sustained to generate 20-40,000 samples in a matter of one to two weeks of effort. During one ten day period, one hundred four (140) 96-well plates of DNA were produced.

[0261] B. Quality Control Methods:

[0262] DNA samples were subjected to quality control (QC) analysis by at least one of two methods: 1) restriction endonuclease digestion and analysis by agarose gel electrophoresis (all plates) or 2) UV spectroscopy to determine DNA quantitation for all 96 samples of a plate (statistical sampling of each days output). For UV analysis, an aliquot of the DNA samples from each plate was taken and measured using a Molecular Dynamics UV spectrometer in 96-well format (Molecular Dynamics, Sunnyvale, Calif.). DNA concentrations of 0.05-0.2 μl with OD 260/280 ratios of 1.7+0.2 are expected. For DNA sequencing purposes (a downstream method to be used to analyze all "hit" samples), DNA quantity of 0.04-0.2 μg/μl is desired. In general, plates that contain >25% of samples not conforming to this metric are rejected and new DNA for the plate must be generated once again. For conformation of the presence of insertions and full-length GENEWARE® vector, agarose gel electrophoresis of restriction endonuclease fragments was used. Aliquots of sixteen samples from each 96-well DNA plate were targeted for restriction digestion using Nco I and BstE II restriction endonucleases. Samples were separated on 1% agarose gels. Generally, plates that showed >25% of samples that were not full length or did not contain insertions were rejected. From a total of 140 96-well DNA plates prepared, 112 passed QC and were made available for generation of infectious units.

[0263] V. High-Throughput DNA Sequencing and Sequence Analysis Protocols

[0264] A. Generation of Raw Sequence Data and Filtering Protocols:

[0265] High-throughput sequencing was carried out using the PCT200® and TETRAD® PCR machines (MJ Research, Watertown, Mass.) in 96-well plate format in combination with two ABI 377™ automated DNA sequencers (PE Corporation, Norwalk, CT). The throughput at present is six 96-well plates per day.

[0266] The electropherogram generated from sequencer by ABI Sequencing Analysis (version 3.3) was used to generate sequence in the text format using "Phred," which also gives a confidence score for each base call that reflect the error probability and the quality for that base. Cross_match was used to mask the vector sequence. The low quality portion of the sequence (i.e. phred score lower than 20) was removed. The vector and the polyA or polyT were also removed from the raw sequence. The high quality, processed sequences with the processing information were stored in the database. Sequences were used for further bioinformatic analysis.

[0267] B. Sequence Data Analysis and Bioinformatics:

[0268] Once the filtering and the vector sequence removal steps are completed, the resulting sequences are subjected to database search. First, low sensitivity methods such as BLASTN and BLASTX can be used. For those sequences that have no hit, more sensitive methods, such as Blimps and Pfam can be used. To speed up the analysis process, appropriate filters may be used. For example, for EST sequences from a given cDNA library sequenced from the 5' end, an ATG filter can be used to make sure that only full-length cDNA will be analyzed. The filtered sequence can be translated in one frame rather than six frames for Pfam analysis.

[0269] The results from the database search are stored in the relational database and can be used for further analysis. For example, all the BLAST results can be stored in a relational table that contains Query, Score, pValue, Hit, Length, Annotation, Frame, Identity, Homology, Query Length, Subject Length, Database Queried and Method used to analyze. Any result can be queried and analyzed by the fields mentioned. A database link between the analysis result database and the laboratory information management system (LIMS) has been created so that the analysis result can be related to the experimental data.

[0270] C. Metabolic Pathway Analysis:

[0271] Many metabolic pathway databases have been constructed that group proteins based on their roles in a metabolic pathway. The basic identifiers for these proteins are E.C. numbers; therefore, the position of a given enzyme in a metabolic pathway may be determined based on its E.C. number. The E.C. number of a protein can be obtained by its Genbank ID. This approach can be used to assign the corresponding E.C. number to the hits found for each cDNA sequence. By querying the metabolic pathway using the E.C. number of a hit, a potential link between this cDNA sequence and the metabolic pathway may be established. Each link can be used as a building block for a plant metabolic pathway. This potential link between cDNA

sequence and metabolic pathway provides a starting point to analyze the gene's role in a metabolic pathway.

[0272] In addition, we have created an interactive, queriable relational prokaryotic and eukaryotic metabolic pathway database. This metabolic pathway database was created by accessing all public sequences that have associated E.C. numbers, running HMMs (hidden Markov models) and other proprietary LSBC algorithms against these sequences, and classifying these sequences into protein families based on conserved domains (Pfam database assignments). Pfam is a database of multiple alignments of protein domains or conserved protein regions. It is assumed that they represent some evolutionary conserved structure which has implications for the protein's function. Pfam is actually formed in two separate ways. Pfam-A are accurate human crafted multiple alignments whereas Pfam-B is an automatic clustering of the rest of SWISSPROT and TrEMBL derived from the Prodom (http://www.toulouse.inra.fr/prodom.html) database. Each protein family has the following data: 1). A seed alignment which is a hand edited multiple alignment representing the domain; 2). A Hidden Markov Model (HMM) derived from the seed alignment which can be used to find new members of the domain and also take a set of sequences to realign them to the model; 3). A full alignment which is a automatic alignment of all the examples of the domain using the HMM to find and then align the sequences; and 4). An annotation file which contains a brief description of the domain, some parameters for Pfam methods, and links to other databases.

[0273] We have run HMMs and other LSBC algorithms against the LSBC Sequence Database and classified these sequences into protein families based on conserved domains, and relate these sequences back to public sequences for E.C. mapping to metabolic pathways. We have run HMMs and other LSBC algorithms against all sequenced microbial genomes and classified these sequences into protein families based on conserved domains, and relate these sequences back to public sequences for E.C. mapping to metabolic pathways. We further related the Arabidopsis, *N. benthamiana,* and Oryza clones to specific sites on metabolic pathways.

[0274] D. Sequence Analysis of Library Created from GENEWARE® Vectors:

[0275] Five hundred sixty-eight (568) independent clones were sequenced from the virus expression library and the clones from this library were analyzed by vector, N filters and BLAST analysis. Of the 568 initial sequences submitted for analysis, 131 were eliminated by the N-filter indicating that ~15% of the sequence were undetermined Ns. The remaining 437 sequences were then subjected to analysis for duplication within each set of submitted plates. Fifty-five (55) sequences were removed due to this duplication filter. These sequences were BLASTN searched against 539 sequences from the AtwpLNLH library in Lambda Zap II. Thirty percent (30%) of the sequences (i.e., 132 sequences) found a match in both libraries. From the original set of GENEWARE® clones, 305 were found to be unique with respect to the Lambda Zap II library. These sequences were then BLASTX-searched against non-redundant GENBANK . From the 305 submitted sequences, 173 sequences found solid hits in protein coding sequence as determined by hit criteria and 132 were found to be unique. Further BLASTN analysis showed a range of sequence homology, but many represented hits to BAC or chromosomal sequences. A wide range of sequences were found including, ribosomal proteins, photosystem reaction center proteins, fumarase and other general metabolism proteins, transcription factors, kinase homologs, omega-6 fatty acid desaturase and various hypothetical proteins. These results strongly suggest that little or no bias is introduced during the construction of cDNA libraries in GENEWARE®.

[0276] VI. Preparation of Infectious Units

[0277] DNA plates that pass QC testing were then moved to the next stage of the cycle, the generation of infectious units. In vitro RNA transcriptions have been optimized to produce maximal amounts of RNA in smaller volumes to reduce costs and increase the lifetime of a DNA preparation. A transcription mixture containing a 6-to-1 RNA cap structure-to-rGTP ratio, Ambion mMessage Machine buffer and enzyme mix (Ambion, Inc., Austin, Tex.) is delivered to a 96-well plate by the TECAN liquid handling robot (TECAN, Research Triangle Park, N.C.). To this reaction mix, the Robbins Scientific HYDRA 96-sample pipeting robot (Robbins Scientific, Sunnyvale, Calif.) delivers 2 μl of DNA solution. This final transcription reaction is incubated at 37° C. for 1.5 hours. Following incubation, the TECAN robot delivers 95 μl of a 100 mM Na/K PO_4 buffer containing TMV coat protein (devoid of all infectious RNA) to the transcription plate and it is incubated overnight. This incubation generates encapsidated transcripts, which are very stable at room temperature or 4° C. and amplified with regard to number of infectious units per μg of RNA transcript. The generation of infectious materials is measured by inoculation of GFP-expressing virus to systemic host or *Nicotiana tabacum* NN lines, incubation at permissive temperatures and counting of developing local lesions on inoculated leaves. Before addition of the TMV coat protein mixture, 0.5 μl from 8 wells of each transcription plate is removed and analyzed by agarose gel electrophoresis. The presence of an RNA band of ~1.6 to 3.5 kb is strong evidence for a successful transcription. If >25% contain only lower molecular weight RNA bands, or if the band is diffuse <500 bp of dsDNA marker, the transcription plate is considered to have failed and removed from the stream of plates prepared for inoculation. During a two week period, 112 plates were transcribed and 108 plates were passed for plant inoculation in growth rooms and in the field.

[0278] VII. Plant Inoculation with Encapsidated RNA Transcripts

[0279] In order to prepare for plant inoculation, 90 μl of each encapsidated RNA transcript sample and 90 μl of FES transcript inoculation buffer (0.1 M glycine, 0.06 M K_2HPO_4, 1% sodium pyrophosphate, 1% diatomaceous earth and 1% silicon carbide) were combined in the wells of a new 96-well plate. The 96 well plate was then placed on ice.

[0280] *Nicotiana benthamiana* plants 14 days post sowing were removed from the greenhouse and brought into the laboratory. Humidity domes were placed over the plants to retain moisture. The RNA transcript sample was mixed by pipetting the solution prior to application to ensure that the silicon carbide and the diatomaceous earth were resuspended. The entire sample, 180 μl, was drawn up and pipetted in equal aliquots (approximately 30 μl), onto the

first two true leaves of three separate *Nicotiana benthamiana* plants. The mixture was spread across the leaf surface using a Texwipe™ Cleanfoam™ swab (The Texwipe Co, Upper Saddle River, N.J.). The wiping action caused by the swab together with the silicon carbide in the buffer sufficiently abrades the leaves so as to allow the encapsidated RNA transcript to enter the plant cell structure. Other methods used for inoculation have included pipeting of encapsidation-FES mixture onto leaves and rubbing by hand, cotton swab or nylon inoculation wand. Alternatively, nylon inoculation wands may be incubated in the transcript-FES mixture for ~30 min to soak up ~15 μl and then rubbed directly onto the leaves.

[0281] Once an entire 32 plant flat was inoculated, the plants were misted with deionized water and the humidity domes were replaced over them. The inoculated plants were retained in the laboratory for 6 hours and then returned to the greenhouse. Once in the greenhouse, the humidity domes were removed and the plants were misted a second time with deionized water.

[0282] VIII. Inoculated Plant Growth

[0283] Plants inoculated with encapsidated virus were grown in a greenhouse. Day length was set to 16 hours and shade curtains (33% transmittance) were used to reduce solar intensity. Whenever ambient light fell below 250 μmol m^2s^{-1}, a 50:50 mixture of metal halide and sodium halide lamps (Sylvania), delivering an irradiance of approximately 250 μmol m^2s^{-1}, were used to provide supplemental lighting. Evaporative cooling and steam heat were used to regulate temperature, with a daytime set point of 27° C. and a nighttime set point of 22° C. The plants were irrigated with Hogland's fertilizer mix as required. Drainage water was collected and treated with 0.5% sodium hypochlorite for 10 minutes before discharging into the municipal sewer.

[0284] To allow space for increased plant size, the inoculated *N. benthamiana* were repositioned at seven days post-inoculation (dpi) so that they occupied twice their original area. At 13 dpi, the plants were examined visually for symptoms of TMV infection and were assigned a numerical score to indicate the extent of viral infection (0=no infection, 1=possible infection, 2=limited/late infection, 3=typical infection, 4=severe infection). At the same time, the plants were assigned a fate for harvest (typically the highest quality plant in each triplicate was assigned to metabolic screens and the second highest quality plant was assigned to focused screens). In cases where plant symptoms deviated substantially from those of plants inoculated with control vectors, a description of plant phenotype was recorded (as described below). At 14 dpi infected plants were harvested.

[0285] IX. Infectivity Analysis

[0286] The method to measure the infectivity of the transcript encapsidations was to inoculate a set of 96-well plates from both positive and negative sense clones and look for systemic virus movement and phenotype development. Of the 8,352 plants inoculated with unique encapsidated transcriptions, 6,266 became systemically infected for an infection rate of 76%. Overall, the majority of plates generated showed very good infection rates. As shown in a graph of the number of systemically infectious constructs per each individual plate plotted against plate number. The majority of plates had systemic rates >70% with one at 100%. Approximately 25 plates had infection rates ranging between 40 and 70% while only 6% (>5 plates) showed infection rates <45%.

[0287] A population of constructs did not show systemic infection on *Nicotiana benthamiana* plants. Analysis using the LIMS revealed a substantial correlation between a subset of inoculators and the transcription plates showing poor infection rates. These results strongly suggest that inoculation technique is critical for good infectivity although other possible causes could include poor DNA or transcription quality, or simply inoculation error. In some cases the constructs may be restricted to inoculated leaves by way of adverse influence of the gene insertion on virus replication and movement. For example, one observed healthy inoculated *Nicotiana benthamiana* plant exhibited clear chlorotic spots on inoculated leaves, yet no systemic symptoms. Other plants, not scored as infected in our LIMS, were observed to have subliminal infections in source tissues. It was clear that the properties of the genetic insertion had differing effects on virus phenotypic symptoms. Eighty-two of those constructs exhibiting poor systemic infection were re-inoculated into *Nicotiana tobacum* NN plants to test for local lesions. The presence of local lesions indicated infectious viral vectors. From this data, a statistical calculation can be made to determine the percentage of non-systemic infective constructs that are locally infectious. Plants were scored 6 days post-inoculation for the presence of localized necrotic lesions resulting from infection and localized movement of virus vectors on the inoculated leaves of the plants. Of the 82 constructs analyzed, 50 showed local lesions indicating the presence of infectious viral vectors. Based on the infection rate observed in *Nicotiana benthamiana* and NN tobacco plants, we estimate that 1,181 (~61%) of the constructs not showing systemic infection on *Nicotiana benthamiania* plants were still infectious and amenable to biochemical analysis.

[0288] X. Phenotypic Evaluation

[0289] At 13 dpi a visual examination was made to identify plants whose phenotype deviates substantially from plants infected with a GENEWARE® control. The phenotypically different plants were divided into regions (for example: shoot apical region, infected phloem source leaves, stem) and descriptive terms were applied to each region to document the visual observation. Additionally, a confirmation was made as to whether or not the operator considered the plant to be a "hit" and a numerical score was applied to document the phytotoxic/herbicide effect of the RNA insert (1=possible effect, 2=mild, 3=moderate, 4=severe).

[0290] A matrix-style phenotypic database was created using the LIMS software. The LIMS software allows all descriptive terms to be used for any major part of the plant and the capacity of sub-parts to be described. Notable phenotypic events are captured by description of individual plant parts. The matrix is configured in a Web-based page that allows one to score infection and phenotyping using a graphic replicated of the physical arrangement of plants in the growth room. This approach is rapid, allowing 96 plants to be described in detail as being infected, not infected with a detailed phenotype in ~15 min. Editing of output files can occur rapidly in MS Excel if desired. The output file is then loaded as CSV files into the LIMS where it is immediately available to Boolean query as to phenotype descriptors with

"and, or, not" statements. Images of infected plants are linked to the SeqIDs in the database so that the plant tray bar code (for infection), well position, SeqID, phenotype and picture all link together when a query is made. This is linked back to the sequence database for sequence annotation data. Using this system, 8,352 phenotypic observations were made in the period of two days and entered into the LIMS. Hundreds of interesting visual phenotypes were observed.

[0291] XI. Field-Scale Genomics

[0292] The effects of gene overexpression and gene silencing in plants may have dramatic differences when grown under different conditions. The Kentucky field test plots available to Biosource provides an opportunity to subject plants to substantially different growth conditions and thereby broaden the chances of detecting various types of "hits" in a genomics screen. To compare the ability of virus vectors to be applied under field conditions and under controlled growth room conditions, we inoculated, in duplicate, 960 positive-sense constructs on *Nicotiana benthamiana* plants grown in the field test plot in Owensboro, Ky. This activity was concurrent with inoculations and screens performed in Vacaville, Calif. Complete encapsidated transcription reactions were prepared at Large Scale Biology Corporation in Vacaville, Calif. and following incubation with TMV coat protein, FES buffer was added to each well. All samples in column 12 of each plate contained encapsidated transcripts of 1057 vector containing the GFP gene. The mixture was then overnight-mailed to Owensboro, Ky. where it was inoculated onto 4-5 week post-sowing plants by rubbing cotton swabs, pre-wetted by incubation with encapsidated transcript-FES mixture, on plant leaves. Plants were inoculated in duplicate. Plants were allowed to remain in the field for 4 weeks post-inoculation and then subjected to phenotypic analysis. Photographic documentation of the plants both pre- and post-inoculation was prepared. Plants were scored by visual evaluation as to number of infected plants compared with total number of plants inoculated. Of the 1920 plants inoculated, 1,712 (88%) showed systemic infections. More than 100 new phenotypes were noted in the field. Each was compared with the phenotype of the same construct inoculated into plants in Vacaville, Calif. growth rooms. Two new phenotypes are particularly noteworthy: two independent plants showed survival phenotypes under anaerobic conditions, whereas all neighbors had succumbed to root rot in a low spot in the field.

[0293] In order to evaluate the effect of gene silencing in *Nicotiana tabacum* plants, mRNA from *Arabidopsis thaliana* whole plants was subjected to fragment normalization such that small cDNA fragments were produced. The cDNA population showed high degree of normalization by hybridizations with known genes of variable expression and by comparison with non-normalized cDNA fragments. The average size of the normalized fragments in the GENEWARE® vectors was between 400-500 bp allowing facile movement of the recombinant viruses systemically in field *Nicotiana tabacum* c.v. MD609 plants. A total of 11 plates of DNA constructs (1056) were prepared, transcribed and encapsidated with GFP constructs integrated at every 12th position. These were mixed with FES and overnight-mailed to Owensboro, Ky. These 1056 constructs were inoculated in duplicate (2112 total) on MD609 tobacco plants 11 weeks post-sowing. One set of the replicates (1056 plants) were scored by visual evaluation as to number of infected plants compared with total number of plants inoculated. Of the 1056 plants inoculated, 808 showed systemic infections, or 76.5% infection rate. "Hits" were determined by unusual visual symptoms and corresponding constructs will be characterized by DNA sequencing.

[0294] An uncharacterized GENEWARE® library comprised of 20,000 *Arabidopsis thaliana* normalized fragment cDNAs and 10,000 of *Nicotiana benthamiana* genomic DNA fragments was prepared and sprayed as a population on *Nicotiana tabacum* c.v. MD609 plants. The Arabidopsis cDNA library, ~10,000, was constructed by ligation into prepared GENEWARE® vectors and purified from pooled bacterial transformants and followed by pooled transcription. The remaining 10,000 cDNA fragments were individual clones prepared and transcribed independently and then mixed in a pooled encapsidation. The Nicotiana library was a prototype cell-free cloning library from restriction endonuclease fragmented gDNA of <500 bp in size. The number of clones corresponds to an approximation of the amount of DNA undergoing complete ligation. Transcriptions from each non-encapsidated library were inoculated separately into *Nicotiana tabacum* protoplasts and allowed to incubate for three days. Cells were lysed and libraries combined. The pool of cell lysates and encapsidated transcriptions containing viral libraries were shipped to Owensboro, KY where they were inoculated onto *Nicotiana tabacum* c.v. MD609 plants at 1, 1/10, 1/100 and 1/000 dilution of the mixed virion preparation (using 60 ml, 6 mls, 0.6 mls and 0.06 mls of the library respectively). Eight hundred (800) plants were spray-inoculated with each library virion dilution. Plants were visually scored and of the 3,200 plants inoculated, 1,304 showed visual symptoms 3 weeks post-infection. The infectivity rate varied from ~60% for the most concentrated inoculum to ~20% for the most dilute as would be expected due to dilution. Analysis will continue to define "Hits" by unusual visual symptoms and PCR amplification and DNA sequencing will characterize corresponding construct.

[0295] XII. GC/MS Metabolite Analysis

[0296] A. Harvest and Preparation of Tissues for Metabolic Screening

[0297] Fourteen dpi infected plants to be harvested were moved from the greenhouse to the laboratory. Plants were scanned and identified by a bar-code that linked the infected plant to the tissue sample. The infected tissue was cut off of the plant and placed in a corresponding centrifuge tube. A tungsten carbide ball was placed on top of the infected tissue sample. The tungsten carbide ball facilitates pulverization of plant tissue. The tubes and sample were stored on dry ice during the harvesting procedure. The samples were then stored at −70° C. Before conducting a metabolic screen, the tissue samples must be pulverized. The sample tubes were loaded into a KLECO pulverizer and pulverized to create a fine powder of the tissue sample. The tissue sample powder was then weighed out into a metabolic extraction vial.

[0298] B. FAME Analysis Procedure for FAME Screen.

[0299] *Nicotiana benthamiana* plants expressing genes of interest in RNA vectors were grown for 14 dpi as described above. Three leaf disks (0.5 cm in diameter) were placed in cell wells of a borosilicate 96-deepwell plate (Zinsser). 500 μl of heptane was added to each well using a Biomek 2000

Laboratory Automation Workstation. The heptane/tissue samples were stirred on a Bodine magnetic stirrer. After 30 minutes, 50 μl of 0.5N sodium methoxide in methanol was added to each well using the Biomek 2000. After 30 minutes of stirring, 10 μl of water was added to each well. Injections were made directly from the 96-deepwell plate into a Hewlett Packard gas chromatograph (GC) using a LEAP auto injector. The GC method involved a 2 μl injection into a split/splitless injection port using a DB 23 narrow bore column (15 M, 0.25 I.D.). The oven temperature was isothermic at 170° C. The injector temperature was 230° C. and the detector (flame ionization) temperature was 240° C. The run time was 5 minutes, with an equilibration time of 0.5 minutes. The split ratio was 20:1 and the helium flow rate was held at a constant pressure of 19 psi. This GC method allowed for separation and quantification of fatty acid methyl esters which included C16:0,C16:1,C18:0,C18:1, C18:2,and C18:3. Using a dual column GC, four 96-well plates could be sampled in less than 24 hours.

[0300] The following sequences exhibited a positive FAME result (had altered levels of the fatty acids assayed): SEQ ID NOs: 7, 53, and 92. The result of the FAME analysis for SEQ ID NO:92 is shown in Table 5. Table 5 shows the relative percent amounts of fatty acids found in plants transfected with a viral vector comprising SEQ ID NO: 92. An increase in 16:0 fatty acids was observed in 3 of the 5 samples assayed. Table 6 shows the relative percent amounts of fatty acids found in plants transfected with SEQ ID NOs: 7 and 53.

TABLE 5

	FAME Profile									
Sample	16:0	16:1	unk	16:3	unk	18:0	18:1	18:2	18:3	unk
1	24.7	3.4	1.1	3.2	2.6	2.6	3.3	9.2	47.8	2.0
2	20.1	2.9	0.8	4.6	2.9	3.5	7.1	9.2	46.7	2.3
3	17.6	1.8	1.0	3.5	2.9	2.2	6.0	11.8	50.4	2.7
4	23.3	1.9	1.0	3.1	4.6	3.8	8.9	10.6	37.6	5.3
5	23.0	2.6	0.7	3.5	1.6	2.3	3.8	8.1	52.9	1.6
control	19.6	2.8	1.1	3.3	1.8	1.8	3.1	12.0	53.6	1.0
control	18.4	2.7	1.1	3.3	1.7	1.7	3.1	11.3	55.4	1.3

[0301]

TABLE 6

	FAME Profile									
Sample	16:0	16:1	unk	16:3	unk	18:0	18:1	18:2	18:3	unk
SEQ ID NO: 53	23.0	3.5	1.9	2.6	1.7	2	3.3	11.7	49.1	1.3
SEQ ID NO: 7	25.7	3.4	1.3	1.8	0.8	2.3	2.1	8	54.7	0
control	18.7	2.8	1.2	3.8	1.4	1.5	4.2	10.7	55	0.6

[0302] C. Insect Control Bioassays.

[0303] *Nicotiana benthamiana* plants expressing genes of interest in RNA viral vectors were grown for 14 dpi as described previously. Fresh leaf tissue (sample size ~2.5 cm diameter) was excised from the base of infected leaves using a scalpel and placed in insect-rearing tray (Bio RT32, C-D International) wells containing 3 ml of 2% agar. Using a small paintbrush to handle insects, 2 first-instar larvae of tobacco hornworm (Manduca sexta) were placed in each well and trays were sealed using vented covers. Trays were then incubated at 28 C with 48% humidity for 72 hours with a 12-hour photoperiod. Following incubation, samples were scored for mortality and leaf damage according to the following criteria: mortality, 0=0 dead/2 alive; 1=1 dead/1 alive; 2=2 dead/0 alive; leaf damage, 0=0 to 20% leaf consumed; 1=21 to 40% leaf consumed; 2=41 to 60% leaf consumed; 3=61 to 80% leaf consumed; and 4=81 to 100% leaf consumed. Following scoring, insects were weighed on an analytical balance and photographed using a digital camera.

[0304] The following sequences exhibited a positive insect control phenotype: SEQ ID NOs: 3, 5, 7, 27, 32, 37, 59, 80, 92, 103, 106, 108, 109, 110, and 111.

[0305] D. Carbohydrate Screen.

[0306] The dry residue was transferred from the extracting cartridge (10-20 mg) into a 100×13 mm glass tube containing 0.5 ml of 0.5 N HCI in methanol and 0.12 ml of methyl acetate and then sealed (Teflon coated screw cap) under nitrogen and heated for 16 hours at 80° C. The liquid phase was then transferred using an 8-channel pipetter (Matrix) to a glass insert supported by a 96 well aluminum block plate (Modem Metal Craft) and evaporated to dryness (Concentrator Evaparray). The methyl-glycosides and methyl-glycoside methyl esters were silylated in 0.1 ml pyridine and 0.1 ml BSTFA+1% TMCS at room temperature for one hour. The sample generated was analyzed on a DB 1 capillary column (15 meters) with an 11 minute program temperature (from 160° C. to 190° C. at 5° C./min and 190° C. to 298° C. at 36° C./minute and hold 2 minutes) and 3 minutes equilibration time. The following components of the plant

cell wall were identified in the tobacco sample: arabinose, rhamnose, xylose, galactose, galacturonic acid, mannose, glucuronic acid and glucose.

[0307] E. GC/MS Metabolite Analysis:

[0308] A 3 mm tungsten carbide ball bearing was placed into each well of a 96-well deep well block and 300 μl of grinding buffer (2 mM NaOH, 1 mM PMSF, 10 mM beta-mercaptoethanol, and deuterium-labeled compounds) was added to each well. A 13 mm circle (~20 mg) leaf disc plug from ~4 week old *Nicotiana benthamiana* (2 week post-inoculation) apical leaves were placed into the 96-well microtiter deepwell plate. The plate was tightly sealed and placed on a mechanical shaker (paint mixer, up to four at a time) for 2 min, then rotated 180° and shaken for an additional 2 min. Subsequently, the samples were spun for 10 min at 3200 RPM in a refrigerated (15° C.) centrifuge equipped for microtiter plates. Following centrifugation, the 96-well plate containing the homogenized samples was placed on a TECAN GENESIS RSP 200 (TECAN, Research Triangle Park, N.C.) liquid handler/robotics system. Both Logic and Gemini software were used to control the TECAN liquid handler. Approximately 200 μl was transferred to a pre-conditioned (1 ml MeOH followed by 1 ml of distilled deionized H_2O) Waters 96-well Oasis HLB solid phase extraction (SPE) plate by the TECAN liquid handler for metabolite analysis by GC/MS. The Waters Extraction Plate Manifold Kit and a vacuum not greater than 5 mm Hg was used to aspirate plant samples from SPE plate into a waste reservoir. The SPE plate was then washed with 1 ml of 5% MeOH in H_2O by aspirating into waste reservoir and compounds eluted from SP resin with 350 μl of MeOH into a 96-well collection plate. Samples were then transferred to GC autosampler vials, capped and stored in the freezer at 80° C. for metabolite analysis.

[0309] An internal standard solution was prepared by making a stock solution at a concentration of 1 μl (using compound density). Grinding buffer (2 mM NaOH above) with the internal standard was prepared at a concentration of 10 ng/μl for each (3,000 ng/300 μl) to yield a concentration equivalent of approximately 150 ng/mg wet weight of plant tissue. Following extraction of plant material, this solution was transferred to the SPE plate by the TECAN liquid handler and extracted with 350 μl of MeOH. Approximately 20 μl of the sample will be injected onto a 30 m×0.32 mm DB-WAX (1 μm film thickness) GC column with a large volume injector during the preliminary study. The GC column oven was temperature held at 35 C for 5 min, then programmed at 2.5° C./min to 250° C. and held for 15 min.

[0310] Samples that contained peaks that were present in altered levels relative to control samples as identified from chromatograms were further analysis using mass spectroscopy. Samples that were transfected with the following nucleic acid sequences were found to have altered metabolic profiles: SEQ ID NO: 43, 50, 81, 85, and 92. Table 7 shows the retention time and % change in peaks relative to controls for several sequences. Table 7 also shows the identity of the peaks as determined by mass spectroscopy.

TABLE 7

Metabolic Profiles

SEQ ID NO	RT (MIN)	% Change	Compound
43	10.68	+130	Malic Acid
43	11.63	+250	Ribonic Acid; Gamma-lactone
43	12.93	+260	Quinic Acid
43	14.12	+120	Inositol
81	10.67	+300	Malic Acid
81	10.87	+150	L-Aspartic Acid
81	10.92	+80	5-Oxo-L-Proline (pyroglutamic)
81	12.48	+100	Ribonic Acid
81	12.64	+800	Citric Acid
81	16.44	+60	Sucrose
92 FA	9.31	−95	Dodecanoic Acid (12:0)
92 FA	10.28	−90	Myristic Acid (14:0)
92 FA	11.20	+500	Hexadecenoic Acid (16:1)
92 FA	11.96	+200	Oleic Acid (18:1)
92	10.68	+700	Malic Acid
92	11.63	+300	Ribonic Acid; Gamma-lactone
92	12.33	+300	Phosphoric Acid
92	12.65	−1400	Citric Acid
92	12.93	+500	Quinic Aci
92	14.12	+800	Inositol
50	11.0	New	
50	11.7	New	

[0311] A 3 mm tungsten carbide ball bearing was placed into each well of a 96-well deep well block and 300 μl of grinding buffer (2 mM NaOH, 1 mM PMSF, 10 mM beta-mercaptoethanol, and deuterium-labeled compounds) was added to each well. A 13 mm circle (~20 mg) leaf disc plug from ~4 week old *Nicotiana benthamiana* (2 week post-inoculation) apical leaves were placed into the 96-well microtiter deepwell plate. The plate was tightly sealed and placed on a mechanical shaker (paint mixer, up to four at a time) for 2 min, then rotated 180° and shaken for an additional 2 min. Subsequently, the samples were spun for 10 min at 3200 RPM in a refrigerated (15° C.) centrifuge equipped for microtiter plates. Following centrifugation, the 96-well plate containing the homogenized samples was placed on a TECAN GENESIS RSP 200 (TECAN, Research Triangle Park, N.C.) liquid handler/robotics system. Both Logic and Gemini software were used to control the TECAN liquid handler. Approximately 200 μl was transferred to a pre-conditioned (1 ml MeOH followed by 1 ml of distilled deionized H_2O) Waters 96-well Oasis HLB solid phase extraction (SPE) plate by the TECAN liquid handler for metabolite analysis by GC/MS. The Waters Extraction Plate Manifold Kit and a vacuum not greater than 5 mm Hg was used to aspirate plant samples from SPE plate into a waste reservoir. The SPE plate was then washed with 1 ml of 5% MeOH in H_2O by aspirating into waste reservoir and compounds eluted from SP resin with 350 μl of MeOH into a 96-well collection plate. Samples were then transferred to GC autosampler vials, capped and stored in the freezer at −80° C. for metabolite analysis.

[0312] XIII. Protein Profiling by MALDI-TOF

[0313] Approximately 14 days post-inoculation, 960 different *N. benthamiana* leaf plugs transfected with encapsidated virion from a GENEWARE® expression library from growth rooms and 38 from *N. benthamiana* infected in Owensboro, Ky. were collected and the soluble proteins

extracted with a high throughput micro-extraction technique described below. An aliquot of this solution was automatically diluted with matrix by a liquid handler in preparation for analysis by MALDI-TOF mass spectrometry for proteins.

[0314] A. Sample Preparation by High Throughput Micro-Extraction:

[0315] A 3 mm tungsten carbide ball bearing was placed into each well of a 96-well deep well block and 300 μl of grinding buffer (2 mM NaOH, 1 mM PMSF, 10 mM beta-mercaptoethanol, and deuterium-labeled compounds-GC/MS analysis) was added to each well. A 13 mm circle (~20 mg) leaf disc plug from ~4 week old *Nicotiana benthamiana* (2 week post-inoculation) apical leaves were placed into the 96-well microtiter deepwell plate. The plate was tightly sealed and placed on a mechanical shaker (paint mixer, up to four at a time) for 2 min, then rotated 180° and shaken for an additional 2 min. Subsequently, the samples were spun for 10 min at 3200 RPM in a refrigerated (15° C.) centrifuge equipped for microtiter plates. Following centrifugation, the 96-well plate containing the homogenized samples was placed on a TECAN GENESIS RSP 200 (TECAN, Research Triangle Park, N.C.) liquid handler/robotics system. Both Logic and Gemini software were used to control the TECAN liquid handler. Samples were diluted by the TECAN liquid handler in a round bottom 96-well plate for MALDI-TOF analysis by adding 18 μl of sinapinic acid matrix and 2 μl of plant extract to each well. Samples were mixed well by aspirating/dispensing 10 μl volumes five times. A 2 μl aliquot of each sample was spotted onto a 100 sample MALDI plate. In addition, a 5.0 μl aliquot of each sample was transferred to a 96-well microtiter plate for PCR and/or MALDI backup analysis and stored at −80° C. Two plant trays containing 96 individually infected each were extracted each day for 5 days.

[0316] B. MALDI-TOF Mass Spectrometry Analysis:

[0317] An aliquot of the homogenized plant samples were diluted 1 :10 with sinapinic acid (Aldrich, Milwaukee, Wis.) matrix, 2 μl applied to a stainless steel MALDI plate surface and allowed to air dry for analysis. The sinapinic acid was prepared at a concentration of 10 mg/ml in 0.1% TFA/acetonitrile (70/30) by volume. MALDI-TOF mass spectra were obtained with a PerSeptive Biosystems Voyager DE-PRO operated in the linear mode. A pulsed nitrogen laser operating at 337 nm was used in the delayed extraction mode for ionization. An acceleration voltage of 25 kV with a 90% grid voltage and a 0.1% guide wire voltage was used. Approximately 150 scans were acquired and averaged over the mass range of 2000-156,000 Da. with a low mass gate of 2000. Ion source and mirror pressures were approximately 2.2×10^{-7} and 8×10^{-8} Torr, respectively. All spectra were mass calibrated with a single-point fit using horse apomyoglobin (16,952 Da).

[0318] C. Results:

[0319] This study describes a method that was developed using the high-throughout capabilities of MALDI-TOF MS to detect changes in total protein profiles of crude plant extracts derived from a GENEWARE® cDNA library. As many as 192 samples per day were extracted and analyzed for protein profiling using MALDI-TOF mass spectrometry. In addition, the method has been optimized in house for detection of a wide range of protein masses from one MALDI-TOF scan. More than 50 proteins were routinely detected in a MALDI profile spectrum ranging from approx. 3,000 to 110,000 Da. In addition to the coat protein (~17,500 Da), both small (~14,500 Da) and large (~52,750 Da) subunits of RuDP carboxylase were routinely detected in the plant samples. Several other proteins were common to most of the plants analyzed. The most abundant proteins were observed at around 3,386, 3,970, 4,408, 5,230, 7,280 (doubly charged ion for small sub-unit of RuDP carboxylase), 8,334, 9,350, 10,450 (most abundant protein overall), 14,020, 18,006, 19,628, 20,286, 21,173, 24,014, 25,124 and 29,140 (dimer of small sub-unit) daltons. A series of less abundant proteins were also detected. Up-regulated or novel proteins were detected in 17.3% of the 960 spectra that were analyzed. This data was entered into the LIMS database.

[0320] XIV. ABRC Library Construction in GENEWARE Expression Vectors

[0321] Expressed sequence tag (EST) clones were obtained from the Arabidopsis Biological Resource Center (ABRC; The Ohio State University, Columbus, Ohio 43210). These clones originated from Michigan State University (from the labs of Dr. Thomas Newman of the DOE Plant Research Laboratory and Dr. Chris Somerville, Carnegie Institution of Washington) and from the Centre National de la Recherche Scientifique Project (CNRS project; donated by the Groupement De Recherche 1003, Centre National de la Recherche Scientifique, Dr. Bernard Lescure and colleagues). The clones were derived from cDNA libraries isolated from various tissues of *Arabidopsis thaliana* var Columbia. A clone set of 11,982 clones was received as glycerol stocks arrayed in 96 well plates, each with an ABRC identifier and associated EST sequence.

[0322] An ORF finding algorithm was performed on the EST clone set to find potential full-length genes. Approximately 3,200 full-length genes were found and used to make GENEWARE constructs in the sense orientation. Five thousand of the remaining clones (not full-length) were used to make GENEWARE constructs in the antisense orientation.

[0323] Full-length clones used to make constructs in the sense orientation were grown and DNA was isolated using Qiagen (Qiagen Inc., Valencia, Calif. 91355) mini-preps. Each clone was digested with NotI and Sse 8387 eight base pair enzymes. The resultant fragments were individually isolated and then combined. The combined fragments were ligated into pGTN P/N vector (with polylinker extending from PstI to NotI −5' to 3'). For each set of 96 original clones approximately 192 colonies were picked from the pooled GENEWARE ligations, grown until confluent in deep-well 96-well plates, DNA prepped and sequenced. The ESTs matching the ABRC data was bioinformatically checked by BLAST and a list of missing clones was generated. Pools of clones found to be missing were prepared and subjected to the same process. The entire process resulted in greater than 3,000 full-length sense clones.

[0324] The negative sense clones were processed in the same manner, but ligated into pGTN N/P vector (with polylinker extending from NotI to PstI −5' to 3'). For each set of 96 original clones approximately 192 colonies were picked from the pooled geneware ligations and DNA prepped. The DNA from the GENEWARE ligations was subjected to RFLP analysis using TaqI 4 base cutter. Novel

patterns were identified for each set. The RFLP method was applied and only applicable for comparison within a single ABRC plate. This procedure resulted in greater than 6,000 negative sense clones.

[0325] The identified clones were re-arrayed, transcribed, encapsidated and used to inoculate plants.

[0326] XV. Inoculation of Plants

[0327] A. Plant Growth.

[0328] *N. benthamiana* seeds were sown in 6.5 cm pots filled with Redi-earth medium (Scotts) that had been pre-wetted with fertilizer solution (prepared by mixing 147 kg Peters Excel 15-5-15 Cal-Mag (The Scotts Company, Marysville Ohio), 68 kg Peters Excel 15-0-0 Cal-Lite (15% Ca), and 45 kg Peters Excel 10-0-0 MagNitrate (10% Mg) in hot tap water to 596 liters total volume and then injecting this concentrate into irrigation water using an injection system (H. E. Anderson, Muskogee Okla.), at a ratio of 200:1). Seeded pots were placed in the greenhouse for 1 d, transferred to a germination chamber, set to 27° C., for 2 d (Carolina Greenhouses, Kinston, N.C.), and then returned to the greenhouse. Shade curtains (33% transmittance) were used to reduce solar intensity in the greenhouse and artificial lighting, a 1:1 mixture of metal halide and high pressure sodium lamps (Sylvania) that delivered an irradiance of approximately 220 μmol m^2s^{-1}, was used to extend day length to 16 h and to supplement solar radiation on overcast days. Evaporative cooling and steam heat were used to regulate greenhouse temperature, maintaining a daytime set point of 27° C. and a nighttime set point of 22° C. At approximately 7 days post sowing (dps), seedlings were thinned to one seedling per pot and at 17 to 21 dps, the pots were spaced farther apart to accommodate plant growth. Plants were watered with Hoagland nutrient solution as required. Following inoculation, waste irrigation water was collected and treated with 0.5% sodium hypochlorite for 10 minutes to neutralize any viral contamination before discharging into the municipal sewer.

[0329] B. Innoculation.

[0330] For each GENEWARE™ clone, 180 μL of inoculum was prepared by combining equal volumes of encapsidated RNA transcript and FES buffer (0.1M glycine, 0.06 M K_2HPO_4, 1% sodium pyrophosphate, 1% diatomaceous earth (Sigma), and either 1% silicon carbide (Aldrich), or 1% Bentonite (Sigma)). The inoculum was applied to three greenhouse-grown *Nicotiana benthamiana* plants at 14 or 17 days post sowing (dps) by distributing it onto the upper surface of one pair of leaves of each plant (30 μL per leaf). Either the first pair of leaves or the second pair of leaves above the cotyledons was inoculated on 14 or 17 dps plants, respectively. The inoculum was spread across the leaf surface using one of two different procedures. The first procedure utilized a Cleanfoam swab (Texwipe Co, N.J.) to spread the inoculm across the surface of the leaf while the leaf was supported with a plastic pot label (¾×5 2M/RL, White Thermal Pot Label, United Label). The second implemented a 3" cotton tipped applicator (Calapro Swab, Fisher Scientific) to spread the inoculum and a gloved finger to support the leaf. Following inoculation the plants were misted with deionized water.

[0331] C. Infection.

[0332] At 13 days post inoculation (dpi), the plants were examined visually and a numerical score was assigned to each plant to indicate the extent of viral infection symptoms. 0=no infection, 1=possible infection, 2=infection symptoms limited to leaves<50-75% fully expanded, 3=typical infection, 4=atypically severe infection, often accompanied by moderate to severe wilting and/or necrosis.

[0333] XVI: Phenotypic Evaluation

[0334] At 13 dpi plants were examined and in cases where a plant's visual phenotype deviated substantially from the phenotypes of control plants, a controlled vocabulary utilizing a five-part phrase was used to describe the plants. Phrase: plant region/sub-part/modifier (optional)/symptom/severity. Plant regions: sink leaves (the upper region of the plant considered to be primarily phloem sink tissue at the time of evaluation), source leaves (expanded, fully-infected leaves considered to be phloem source tissue at the time of evaluation), bypassed leaves (leaves [three and four] that display little or no infection symptoms), inoculated leaves (leaves one and two), stem. Subparts: blade, entire, flower, foci, intervein, leaf, lower, major vein, margin, minor vein, node, petiole, shoot apex, upper, vein, viral path. Modifiers: apical, associated, banded, basal, blotchy, bright, central, crinkled, dark, epinastic, flecked, glossy, gray, hyponastic, increased, intermittent, large-spotted, light, light-colored, light-green, mottled, narrowed, orange, patchy, patterned, radial, reduced, ringspot, small-spotted, smooth, spotted, streaked, subtending, uniform, unusual, white. Symptoms: bleaching, chlorosis, color, contortion, corrugation, curling, dark green, elongation, etching, hyperbranching, mild symptoms, necrosis, patterning, recovery, stunting, texture, trichomes, wilting. Severity: 1—extremely mild/trace, 2—mild symptom (<30% of subpart affected), 3—moderate symptom (30%-70% of subpart affected), 4—severe symptom (>70% of subpart affected). Based on the symptoms a phenotypic hit value (PHV) and a herbicide hit value (HHV) were assigned to each plant phenotyped. Phenotype Hit Value: 1—no predicted value; do not request for repeat analysis, 2—of uncertain value, 3—of potential value; strong phenotype, 4—highly unusual phenotype. Herbicide Hit Value: 1—no predicted value; do not request for repeat analysis, 2—of uncertain value, 3—moderate chlorosis (especially in apical region) or necrosis, 4—Severe phytotoxicity/herbicide mode of action. Comments were added if additional information was required to complete the plant characterization. Results are presented in Table 8.

TABLE 8

SEQ ID NO	Library	Summary of Visual Phenotype
SEQ ID NO:12	ABRC	Stunting
SEQ ID NO:27	ABRC	Stunting
SEQ ID NO:48	ABRC	Stunting
SEQ ID NO:49	ABRC	Stunting
SEQ ID NO:59	ABRC	Stunting
SEQ ID NO:60	ABRC	Stunting
SEQ ID NO:71	ARAB	Stunting
SEQ ID NO:84	ABRC	Stunting
SEQ ID NO:99	ABRC	Stunting
SEQ ID NO:100	ABRC	Stunting
SEQ ID NO:102	ABRC	Stunting
SEQ ID NO:103	ABRC	Stunting
SEQ ID NO:105	ABRC	Stunting

TABLE 8-continued

SEQ ID NO	Library	Summary of Visual Phenotype
SEQ ID NO:106	ABRC	Stunting
SEQ ID NO:107	ABRC	Stunting
SEQ ID NO:108	ABRC	Stunting
SEQ ID NO:109	ABRC	Stunting
SEQ ID NO:110	ABRC	Stunting

[0335] XVII: Metabolic Screens

[0336] A. Sample Generation.

[0337] Individual dwarf tobacco *nicotiana benthamiana*, (Nb) plants were manually transfected with an unique DNA sequence at 14 or 17 days post sowing using the GENEWAREETM viral vector technology (1). Plants were grown and maintained under greenhouse conditions. At 13 days after infection, an infection rating of 0, 1, 2, 3, or 4 was assigned to each plant. The infection rating documents the degree of infection based on a visual observation. A score of 0 indicates no visual infection. Scores of 1 and 2 indicate varying degrees of partial infection. A score of 4 indicates a plant with a massive overload of infection, the plant is either dead or near death. A score of 3 indicates optimum spread of systemic infection.

[0338] Samples were grouped into sets of up to 96 samples per set for inoculation, harvesting and analysis. Each sample set (SDG) included 8 negative control (reference samples), up to 80 unknown (test) samples, and 8 quality control samples.

[0339] B. Harvesting.

[0340] At 14 days after infection, infected leaf tissue, excluding stems and petioles, was harvested from plants with an infection score of 3. Infected tissue was placed in a labeled, 50-milliliter (mL), plastic centrifuge tube containing a tungsten carbide ball approximately 1 cm in diameter. The tube was immediately capped, and dipped in liquid nitrogen for approximately 20 seconds to freeze the sample as quickly as possible to minimize degradation of the sample due to biological processes triggered by the harvesting process. Harvested samples were maintained at −80 C between harvest and analysis. Each sample was assigned a unique identifier, which was used to correlate the plant tissue to the DNA sequence that the plant was transfected with. Each sample set was assigned a unique identifier, which is referred to as the harvest or meta rack ID.

[0341] C. Extraction.

[0342] Prior to analysis, the frozen sample was homogenized by placing the centrifuge tube on a mechanical shaker. The action of the tungsten carbide ball during approximately 30 seconds of vigorous shaking reduced the frozen whole leaf tissue to a finely homogenized frozen powder. Approximately 1 gram of the frozen powder was extracted with 7.5 mL of a solution of isopropanol (IPA):water 70:30 (v:v) by shaking at room temperature for 30 minutes.

[0343] D. Fractionation.

[0344] A 1200 microliter (μL) aliquot of the IPA:water extract was partitioned with 1200 μL of hexane. The hexane layer was removed to a clean glass container. This hexane extract is referred to as fraction 1 (F1). A 90 μL aliquot of the hexane extracted IPA:water extract was removed to a clean glass container. This aliquot is referred to as fraction 4 (F4). The remaining hexane extracted IPA:water extract is referred to as fraction 3 (F3). A 200 μL aliquot of the IPA:water extract was transferred to a clean glass container and referred to as fraction 2 (F2). Each fraction for each sample was assigned a unique aliquot ID (sample name).

[0345] E. Sample Preparation & Data Generation

[0346] Fraction 1:

[0347] The hexane extract was evaporated to dryness under nitrogen at room temperature. The sample containers were sealed and stored at 4 C prior to analysis, if storage was required. Immediately prior to capillary gas chromatographic analysis using flame ionization detection (GC/FID), the F1 residue was reconstituted with 120 μL of hexane containing pentacosane and hexatriacontane which were used as internal standards for the F1 analyses. The chromatographic data files generated following GC separation and flame ionization detection were named with the fraction 1 aliquot ID for each sample and stored in a folder named after the harvest rack (sample set) ID. **FIG. 1 a** summarizes the GC/FID parameters used to analyze fraction 1 samples.

[0348] Fraction 2:

[0349] The F2 aliquot was evaporated to dryness under nitrogen at room temperature and reconstituted in heptane containing 2 internal standards, C11:0 and C24:0. In general, fraction 2 is designed to analyze esterified fatty acids, such as phospholipids, triacylglycerides, and thioesters. In order to analyze these compounds by GC/FID, they were transmethylated to their respective methyl esters by addition of sodium methoxide in methanol and heat. Excess reagent was quenched by the addition of a small amount of water, which results in phase separation. The fatty acid methyl esters (FAMEs) were contained in the organic phase. **FIG. 1***b* summarizes the GC/FID parameters used to analyze fraction 1 samples.

[0350] Fraction 3:

[0351] The F3 aliquot was evaporated to dryness under nitrogen at 40 C. In general, the metabolites in this fraction are highly polar and water-soluble. In order to analyze these compounds by GC/FID, the polar functional groups on these compounds were silylated through a 2-step derivatization process. Initially, the residue was reconstituted with 400 μL of pyridine containing hydroxylamine hydrochloride (25 mg/ml) and the internal standard, n-octyl-β-D-glucopyranoside (OXIME solution). The derivatization was completed by the addition of 400 μL of the commercially available reagent (N,O-bis[Trimethylsily] trifluoroacetamide)+1% Trimethylchlorosilane (BSTFA+1% TMCS). The chromatographic data files generated following GC separation and flame ionization detection were named with the fraction 3 aliquot ID for each sample and stored in a folder named after the harvest rack (sample set) ID. **FIG. 1***c* summarizes the GC/FID parameters used to analyze fraction 1 samples.

[0352] Fraction 4:

[0353] The F4 aliquot was diluted with 90 μL of distilled water and 20 μL of an 0.1 N hydrochloric acid solution containing norvaline and sarcosine, which are amino acids

that are used as internal standards for the amino acids analysis. Immediately prior to high performance liquid chromatographic analysis using fluorescence detection (HPLC/FLD), the amino acids in F4 are mixed in the HPLC injector at room temperature with buffered orthophtaldehyde solution, which derivatizes primary amino acids, followed by fluorenyl methyl chloroformate, which derivatizes secondary amino acids. Following HPLC separation and fluorescence detection, chromatographic data files were generated for each sample, named with a sequential number which can be tracked back to the F4 aliquot ID, and stored in a folder named after the harvest rack (sample set) ID. **FIG. 1***d* summarizes the GC/FID parameters used to analyze fraction 1 samples.

[**0354**] F. Data Analysis & Hit Detection.

[**0355**] Two complementary methods were used to identify modifications in the metabolic profile of test samples from reference samples. These data analysis methods are called automated data analysis (ADA) and quantitative data analysis. Each fraction from each sample was analyzed by one or both of these methods to identify hits. If either method identified a fraction as a hit, the sample was called a hit for that fraction. Therefore a sample could be a hit for 1 through 4 fractions.

[**0356**] ADA employs a qualitative pattern recognition approach using ABNORM (U.S. Pat. No. 5,592,402), which is a proprietary software utility of the Dow Chemical Company. ADA was performed on chromatograms from all 4 fractions. The ADA process developed a statistical model from chromatograms that ideally depict unaltered (reference) metabolic profiles. This model was then used to identify test sample chromatograms that contain statistically significant differences from the normal (control) chromatograms. Updated models for each fraction were generated for each sample set. Chromatograms identified as hits by ADA, were manually reviewed and the data quality visually verified.

[**0357**] Quantitative data analysis is based on individual peak areas. Quantitative data analysis was applied to specific compounds of interest in fraction 2, fatty acids, and fraction 4, amino acids. The peak areas corresponding to these compounds in these fractions were generated. For fraction 2, the relative percent of the peak areas for the compounds in Table 9 were calculated for each sample. The average ($\bar{x}$) and standard deviation (STD) of the relative % of the peak areas for the individual compounds were calculated from the reference sample chromatograms analyzed within the sample set. The average and STD were used to calculate a range for each compound. Depending on the compound, this range was typically $\bar{x}$+/−3 or 5 STDs. If the relative percent of the peak area from an unknown was outside this range, the compound was considered to be significantly different from the 'normal' level and the sample was identified as a hit for F2. For fraction 4, the concentration, in micrograms/gram was calculated for each of the amino acids listed in Table 9, from calibration standards analyzed at the same time as the test samples. The amino acid concentrations from reference samples were used to calculate the acceptable range from the $\bar{x}$ and STD for each amino acid. If the amino acid concentration for an unknown falls outside this range, the amino acid was considered to be different from normal and sample was identified as a hit for F4.\

TABLE 9

Tobacco Metabolites Monitored in Fractions 2 and 4 by Quantitative Analysis

Fraction 2 (Fatty Acids)		Fraction 4 (Amino Acids)	
undecanoic acid methyl ester*	C11:0	Aspartic Acid	ASP
Pentadecanoic acid methyl ester**	C15:0	Glutamic Acid	GLU
Pentadecanoic acid ethyl ester**	C15:0	Serine	SER
palmitic acid methyl ester	C16:0	Histidine	HIS
palmitoleic acid methyl ester	C16:1	Glycine	GLY
iso methylpentadecanoic acid methyl ester	C16:0:Me	Threonine	THR
palmitoleic acid methyl ester	C16:2	Alanine	ALA
palmitolenic acid methyl ester	C16:3	Arginine	ARG
iso methylhexadecanoic acid methyl ester	C17:0Me	Tyrosine	TYR
Stearic acid methyl ester	C18:0	Cystine	CY2
Oleic acid methyl ester	C18:1	Valine	VAL
Linoleic acid methyl ester	C18:2	Methionine	MET
Linolenic acid methyl ester	C18:3	Norvaline*	NVA
Arachidic acid methyl ester	C20:0	Tryptohane	TRP
Lignoceric acid methyl ester*	C24:0	Phenylalanine	PHE
		Isoleucine	ILE
		Leucine	LEU
		Lysine	LYS
		Sarcosine*	SAR
		Proline	PRO

*Internal Standard
**Surrogate Standard

[**0358**] Shipping Hits.

[**0359**] Any F1, F2, or F3 fractions identified as hits by ADA or quantitative analysis, and the most typical null for each fraction for each sample set as identified by ADA, were sent to the Function Discovery Laboratory (see Example 20) for structural characterization of the specific compounds identified. Samples were sealed, packaged on dry ice and shipped for overnight delivery.

[**0360**] XVIII: Identification of Metabolic Changes

[**0361**] This Example describes the identification of the chemical nature of genetic modifications made in tobacco plants using GENEWARE viral vector technology. The protocols involved the use of gas chromatography/mass spectrometry (GC/MS) for the analyses of three primary fractions obtained from extraction and fractionation processes.

[**0362**] A. Methods.

[**0363**] Major instruments and accessories used included Bioinformatics computer programs, mass spectral libraries, Biotech databases, Nautilus LIMS system (BLIMS; Dow), Biotech Database (eBRAD; Dow), HP Model 6890 capillary Gas Chromatograph (GC; Agilent Technologies), HP Model 5973 Mass Selective Detector (MSD; Agilent Technologies), Auto Sampler and Sample Preparation Station (Leap Technologies), Large Volume Injector system (APEX), Ultra Freezer (Revco), and model LS1006 Barcode Reader (Symbol Technologies).

[**0364**] Samples and corresponding References (also referred to as controls or nulls) were shipped via overnight mail. Samples were removed from the shipping container, inspected for damage, and then placed in a freezer until analysis by GC/MS.

[0365] Samples were received in vials or in titer plates with a bar-coded titer plate (TP) number, also referred to as a Rack Identification number that is used to track the sample in the BLIMS system. The barcode number is used by the FDL to extract from BLIMS pertinent information from ADA (Automated chromatographic pattern recognition Data Analysis) HIT reports and/or QUANT (a quantitative data analysis approach that makes use of individual peak areas of select peaks corresponding to specific compounds of interest in the fatty acid Fraction 2) HIT reports generated by the Metabolic Screening Laboratory. The information in these reports includes the well position of the respective HITs (Samples), the corresponding well position of the Reference, and other pertinent information, such as, aliquot identification. This information is used to generate ChemStation and Leap sequences for FDL analyses.

[0366] Samples were sequenced for analysis in the following order:

TABLE 10

Analysis Order
Solvent Blank
Instrument Performance Standard
Samples and Associated Reference
.
.
.
Performance Standard
Solvent Blank

[0367] Samples were analyzed on GC/MS systems using the following procedures. Fraction 1 samples were shipped dry and required a hexane reconstitution step. Fraction 2 and Fraction 3 samples were analyzed as received. Internal standards were added to the samples prior to analysis.

[0368] B. Fraction 1 Analysis.

[0369] The name of the GC/MS method used is BIONEUTx (where x is a revision number of the core GC/MS method). The method is retention-time locked to the retention time of pentacosane, an internal standard, using the ChemStation RT Locking algorithm.

Internal Standard(s)	
Pentacosane	
Hexatriacontane	
Chromatography	
Column:	J & W DB-5MS
	50 M × 0.320 mm × 0.25 μm film
Mode: constant flow	
	Flow: 2.0 mL/min
	Detector: MSD
	Outlet psi: vacuum
Oven:	40° C. for 2.0 min
	20° C./min to 350° C., hold 15.0 min
	Equilibration time: 1 min
Inlet:	Mode: split
	Inj Temp: 250° C.
	Split ratio: 50:1
	Gas Type: Helium
LEAP Injector:	
Injector:	Inj volume: optimized to pentacosane peak intensity (typically 20 μL)
	Sample pumps: 2
	Wash solvent A: Hexane
	Wash solvent B: Acetone
	Preinj Solvent A washes: 2
	Preinj Solvent B washes: 2
	Postinj Solvent A washes: 2
	Postinj Solvent B washes: 2
APEX Injector	
Method Name:	BIONEUTx (where x is a revision number of the core APEX method).
Modes:	Initial: Standby (GC Split)
	Splitless: (Purge Off) 0.5 min
	GC Split: (Standby) 4 min
	ProSep Split: (Flow Select) 23 min
Temps: 50° C. for 0.0 min.	
	300° C./min to 350° C., hold for 31.5 min
Mass Spectrometer	
Scan: 35–800	Da at sampling rate 2 (1.96 scans/sec)
	Solvent delay: 4.0 min
Detector:	EM absolute: False
	EM offset: 0
Temps:	Transfer line: 280° C.
	Ion source: 150° C.
	MS Source: 230° C.

[0370] C. Fraction 2 Analysis:

[0371] The name of the GC/MS method used is BIOFAMEx (where x is a revision number of the core GC/MS method). The method is retention-time locked to RT of undecanoic acid, methyl ester, an internal standard, using the ChemStation RT Locking algorithm.

Internal Standard(s)	
Undecanoic acid, methyl ester	
Tetracosanoic acid, methyl ester	
Chromatography	
Column:	J & W DB-23 FAME
	60 M × 0.250 mm × 0.15 μm film
	Mode: constant flow
	Flow: 2.0 mL/min
	Detector: MSD
	Outlet psi: vacuum
Oven:	50° C. for 2.0 min
	20° C./min to 240° C., hold 10.0 min
	Equilibration time: 1 min
Inlet:	Mode: split
	Inj Temp: 240° C.
	Split ratio: 50:1
	Gas Type: Helium
LEAP Injector:	
Injector:	Inj volume: optimized to undecanoic acid, methyl ester peak intensity (Typically 10 μL)
	Sample pumps: 2
	Wash solvent A: Methanol
	Wash solvent B: Methanol
	Preinj Solvent A washes: 2
	Preinj Solvent B washes: 2
	Postinj Solvent A washes: 2
	Postinj Solvent B washes: 2
APEX Injector	
Method Name:	BIOFAMEx (where x is a revision number of the core APEX method).

-continued

Modes:	Initial: GC Split Splitless: 0.5 min GC Split: 4 min
ProSep Split:	21 min
Temps:	60° C. for 0.5 min. 300° C./min to 250° C., hold for 20 min 300° C./min to 260° C., hold for 5 min
Mass Spectrometer	
Scan: 35–800	Da at sampling rate 2 (1.96 scans/sec) Solvent delay: 4.5 min
Detector:	EM absolute: False
EM offset: 0	
Temps:	Transfer line: 200° C. Ion source: 150° C. MS Source: 230° C.

[0372] D. Fraction 3 Analysis.

[0373] The name of the GC/MS method used is BIOAQUAx (where x is a revision number of the core GC/MS method). Method is retention-time locked to the RT of n-Octyl-β-D-Glucopyranoside, an internal standard, using the ChemStation RT Locking algorithm.

Internal Standard(s)	
n-Octyl-β-D-Glucopyranoside	
Chromatography	
Column:	Chrompack 7454 CP-SIL 8 60 M × 0.320 mm × 0.25 μm film Mode: constant flow Flow: 2.0 mL/min Detector: MSD Outlet psi: vacuum
Oven:	40° C. for 2.0 min 20° C./min to 350° C., hold 10.0 min Equilibration time: 1 min
Inlet: Mode: split	
	Inj Temp: 250° C. Split ratio: 50:1 Gas Type: Helium
LEAP Injector:	
Injector:	Inj volume: Optimized to n-Octyl-β-D-Glucopyranoside peak intensity
(Typically 2.5 μL)	
	Sample pumps: 2 Wash solvent A: Hexane Wash solvent B: Acetone Preinj Solvent A washes: 2 Preinj Solvent B washes: 2 Postinj Solvent A washes: 2 Postinj Solvent B washes: 2
APEX Injector	
Method Name:	BIQAQUAx (where x is a revision number of the core APEX method).
Modes:	Initial: GC Split Splitless: 0.5 min GC Split: 4 min ProSep Split: 20 min
Temps:	60° C. for 0.5 min. 300° C./min to 350° C., hold for 21.1 min
Mass Spectrometer	
Scan: 35–800	Da at sampling rate 2 (1.96 scans/sec) Solvent delay: 4.0 min
Detector:	EM absolute: False
EM offset: 0	
Temps:	Transfer line: 280° C. Ion source: 150° C. MS Source: 230° C.

[0374] E. Performance Standard:

[0375] Two mixtures were used as instrument performance standards. One standard was run with Fraction 1 and 3 samples and the second was run with Fraction 2 samples. Below is the composition of the standards as well as approximate retention time values observed when run under the GC/MS conditions previously described. These retention time values are subject to change depending upon specific instrument and chromatographic conditions.

TABLE 11

Fraction 1 and 3 Performance Standard

Time	Compound
6.25	dimethyl malonate
7.25	dimethyl succinate
8.15	dimethyl glutarate
8.98	dimethyl adipate
11.06	dimethyl azelate
11.42	hexadecane
11.70	dimethyl sebacate
13.57	eicosane
15.36	tetracosane
16.88	octacosane
18.26	dotriacontane
19.95	hexatriacontane

[0376]

TABLE 12

Fraction 2 Performance Standard

Time	Compound
8.82	undecanoic acid, methyl ester
9.32	dodecanoic acid, methyl ester
10.24	tetradecanoic acid, methyl ester
11.07	hexadecanoic acid, methyl ester
11.84	octadecanoic acid, methyl ester
11.90	oleic acid, methyl ester
12.14	linoleic acid, methyl ester
12.39	linolenic acid, methyl ester
12.60	eicosanoic acid, methyl ester
13.42	docosanoic acid, methyl ester

[0377] F. Data Analysis.

[0378] Sample and Reference data sets were processed using the Bioinformatics computer program Maxwell. The principal elements of the program are 1) Data Reduction, 2) two-dimensional Peak Matching, 3) Quantitative Peak Differentiation (Determination of Relative Quantitative Change), 4) Peak Identification, 5) Data Sorting, and 6) Customized Reporting.

[0379] The program queries the user for the filenames of the Reference data set and Sample data set(s) to compare against the Reference. A complete listing of user inputs with example input is shown below.

TABLE 13

Bioinformatics Analysis

USER QUERY	EXAMPLE USER INPUT
Operator Name	M. Maxwell
Total number of data files to process	5
Which Fraction	3
Reference (Control) File Name	AAPR0020.D
Process a specific RT Range	Y
Specific RT range	6.5–23
Internal Standard Retention Time	14.902
+/– variation in Internal Std. RT	.004
Variation in peak RI, ChemStation	.005
Percent variation in peak RI, Biotech Database	.010
Threshold for determining Area % change	60
Spectral Matching Value (Threshold MS-XCR for peaks to be a match)	.95
Percent to determine LOP-PM* Value	1
Percent to determine LOP-SRT** Value	3
Quality Level for Library (Library match)	80
Subtract Background	Y
Time Range for Background	21.5–22.6
SHORT SUMMARY (y/n, y = no chromatograms)	Y

*LOP-PM - Limit of Processing for Peak Matching
**LOP-SRT - Limit of Processing for Sorting

[0380] The program integrates the Total Ion Chromatogram (TIC) of the data sets using Agilent Technologies HP ChemStation integrator parameters determined by the analyst. The corresponding raw peak areas are then normalized to the respective Internal Standard peak area. It should be noted that before the normalization is performed, the program chromatographically and spectrally identifies the Internal Standard peak. Should the identification of the Internal Standard not meet established criteria for a given Fraction, then the data set will not be further processed and it will be flagged for analyst intervention.

[0381] Peak tables from the Reference and each Sample were generated. The peak tables are comprised of retention time (RT), retention index (RI)—the retention time relative to the Internal Standard RT, raw peak areas, peak areas normalized to the Internal Standard, and other pertinent information.

[0382] The first of two filtering criteria, established by the analyst was then invoked and must be met before a peak is further processed. The criterion is based upon a peak's normalized area. All normalized peaks having values below the Limit of Processing for Peak Matching (LOP-PM), were considered to be "background". These "peaks" were not carried forth for any type of mathematical calculation or spectral comparison.

[0383] In the initial peak-matching step, the Sample peak table was compared to the Reference peak table and peaks between the two were paired based upon their respective RI values matching one another (within a given variable window). The next step in the peak matching routine utilized mass spectral data. Sample and Reference peaks that have been chromatographically matched were then compared spectrally. The spectral matching was performed using a mass spectral cross-correlation algorithm within the Agilent Technologies HP ChemStation software. The cross-correlation algorithm generates an equivalence value based upon spectral "fit" that was used to determine whether the chromatographically matched peaks are spectrally similar or not. This equivalence value is referred to as the MS-XCR value and must meet or exceed a predetermined value for a pair of peaks to be "MATCHED," which means they appear to be the same compound in both the Reference and the Sample. The MS-XCR value can also be used to judge peak purity. This two-dimensional peak matching process was repeated until all potential peak matches were processed. At the end of the process, peaks are categorized into two categories, MATCHED and UNMATCHED.

[0384] A second filtering criterion was next invoked, again based upon the normalized area of the MATCHED or UNMATCHED peak. For a peak to be reported and further processed, its normalized area must meet or exceed the predetermined Limit of Processing for Sorting (LOP-SRT).

[0385] Peaks that are UNMATCHED are immediately flagged as different. UNMATCHED peaks are of two types. There are those that are reported in the Reference but appear to be absent in the Sample (based upon criteria for quantitation and reporting). These peaks were designated in the Analyst Report with a percent change of "–100 percent" and the description "UNMATCHED IN SAMPLE." The second types of peaks are those that were not reported in the Reference (again, based upon criteria for quantitation and reporting) but were reported in the Sample, thus appearing to be "new" peaks. These peaks were designated in the Analyst Report with a percent change of "100 percent" and the description "NEW PEAK UNMATCHED IN NULL."

[0386] MATCHED peaks were processed further for relative quantitative differentiation. This quantitative differentiation is expressed as a percent change of the Sample peak area relative to the area of the Reference peak. A predetermined threshold for change must be observed for the change to be determined biochemical and statistically significant. The change threshold is based upon previously observed biological and analytical variability factors. Only changes above the threshold for change were reported.

[0387] Peaks were then processed through the peak identification process as follows. The mass spectra of the peaks were first searched against mass spectral plant metabolite libraries. The equivalence value assigned to the library match was used as an indication of a proper identification.

[0388] To provide additional confirmation to the identity of a peak, or to suggest other possibilities, library hits were searched further against a Biotechnology database. The Biotechnology database is based on the Access database program from Accelrys (formerly Synopsis) and utilizes Accord for Access (also available from Accelrys) to incorporate chemical structures into the database.

[0389] The Chemical Abstract Services (CAS) number of the compound from the library was searched against those contained in the database. If a match was found, the CAS number in the database was then correlated to the data acquisition method for that record. If the method was matched, the program then compared the retention index (RI), in the Peak Table, of the component against the value contained in the database for that given method. Should the RI's match (within a given window of variability) then the peak identity was given a high degree of certainty. Components in the Sample that are not identified by this process

were assigned a unique identifier based upon Fraction Number and RI (example: F1-U0.555). The unique identifier was used to track unknown components. The program then sorts the data and generates an Analyst Report.

[0390] An Analyst Report is an interim report consisting of PBM algorithm match quality value (equivalence value), RT, Normalized Peak Area, RI (Sample), RI (database) Peak Identification status [peak identity of high certainty (peaks were identified by the program based on the pre-established criteria) or criteria not met (program did not positively identify the component)], Component Name, CAS Number, Mass Spectral Library (containing spectrum most closely matched to that of the component), Unknown ID (unique identifier used to track unidentified components), MS-XCR value, Relative % Change, Notes (MATCHED UNMATCHED), and other miscellaneous information. The Analyst Report was reviewed manually by the analyst who determined what further analysis was necessary. The analyst also generated a modified report, for further processing by the program, by editing the Analyst Report accordingly.

[0391] For Fractions 2 and 3, derivatization procedures were performed prior to analysis to make the certain components more amenable to gas chromatography. Thus, the compound names in the modified analyst report (MAR) were those of the derivatives. To accurately reflect the true components of these fractions, the MAR was further processed using information contained in an additional database. This database cross-references the observed derivatized compound to that of the original, underivatized "parent" compound by way of their respective CAS numbers and replaces derivatives with parent names and information for the final report. In addition, any unidentified components were assigned a "999999-99-9" CAS number.

[0392] The Modified Analyst Report also contains a HIT Score of 0, 1, or 2. The value is assigned by the analyst to the data set of the Sample aliquot based on the following criteria:

[0393] 0 No FDL data on Sample

[0394] 1 FDL data collected; Sample not FDL HIT

[0395] 2 FDL data collected; Sample is FDL HIT

[0396] An FDL HIT is defined as a reportable percent change (modification) observed in a Sample relative to Reference in a component of biochemical significance.

[0397] An electronic copy of the final report is entered into the Nautilus LIMS system (BLIMS) and subsequently into eBRAD (Biotech database). The program also generated a hardcopy of the pinpointed TIC and the respective mass spectrum of each component that was reported to have changed.

[0398] "NQ" and "NEW" are two terms used in the final report. Both terms refer to UNMATCHED peaks whose percent changes cannot be reported in a numerically quantitative fashion. These terms are defined as follows:

[0399] "NQ" is used in the case where there was a peak reported in the Reference for which there was no match in the Sample (either because there was no peak in the Sample or, if there was, the area of the peak did not satisfy the Limit of Processing for Peak Matching). The percent change designation of "−100%" used in the Analyst report is replaced with "NQ".

[0400] "NEW" is used in those situations where a peak was reported in the Sample but for which there was no corresponding match in the Reference (either because there was no peak in the Reference or, if there was, the area of the peak did not satisfy the Limit of Processing for Peak Matching). For these situations, the percent change designation of "100%" used in the Analyst Report is replaced with "NEW". The designation of "NEW" in the final report to a component that is present in the Sample but not in the Reference was necessary to eliminate any ambiguity with the appearance of "100%" for MATCHED peaks. A "100%" designation in the final report exclusively refers to a component with modification that doubled in the Sample relative to the Reference.

[0401] G. Results.

[0402] The results of the metabolic screening revealed that transfection with 55 of the inserts resulted in measurable metabolic changes.

SEQUENCE LISTING

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<213> ORGANISM: Nicotiana benthamiana

<400> SEQUENCE: 1

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gcggtcacat tgttgtccag attcttcctt ctgctctttc ctatcttgct ctcatccctg 240

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tctttaatat tctcaatttg tctacgagga gaggatgata tttcattagc ccagccttca 360

-continued

ttttccgcat tggatattcg actctcctca ttactatatt gcgggtaact gcataataag 420

tgaaccgggg aggtaccatg caacggtgtg gccggtctgc tagagacagg ggtgttgttt 480

cccgatagcc ggccgtgttt cacccgcttt ttcgctgtgt tgtgccagct tctaagagct 540

gttgccacat tatcaccaaa gattataggt ttcattgatg ttcccatctg caaatttcac 600

caaatctctc agcactaatt tatctttata agagtttttg ttgtgaaaag ggaagactag 660

tttagttata gagtacctgt gtgaccaagg cataaagagg gagagtcaca tagctgcaat 720

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tgatccaact tcagatccag accaagaagg agatgacatt gtttttatca tccaaaagaa 540

aatgtggctg acaagtgaaa gcatcagaga tacagagtaa ataaagtttg ccactaagta 600

cacttcttga ttcattttcc ccttcctttt gggattaaga aatacacacc cctaaaggtt 660

tgggagatat cagtttgatt ttgtagtatt tatgatattt atttcttcct tttcttcatt 720

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tccagtaaga catcactgtt accatttcgt aatgtttcga gaagcttcaa aaccgtcaag 180

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gcctttgaga agcttctcat gtctagtttt atcagaagga agaagactaa aatcaatctt 420

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atcggaattg gagctttagt tgccgggtgg ttctgcggtt cgttaatcat tcccatgatt 720

ccgacgtttc tcattcagcc tacatggaca ctcgagctcc taacatcact ggtcgcttat 780

gtgtttttgt ttctttcttg tactttcctc aagtaagtta cgttgtggtt ttatccaaac 840

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tgcaccgttg attcttcata tggaggcaat gttcccacgt tccctcggac gagagtttgg 240

gacccgtaca aacgtctagg agttagtcca tatgcttccg aggaagaaat ctgggcctct 300

cgtaactttc ttttacagca gtacgctgga catgaaagaa gcgaagagtc tatagaagga 360

gcctttgaga agcttctcat gtctagtttt atcagaagga agaagactaa aatcaatctt 420

aaatcaaagt tgaagaagaa agttgaggaa tctcctccgt ggctcaaagc tcttctcgat 480

ttcgttgaaa tgcctcccat ggacactatt ttcagaagac ttttcctctt tgccttcatg 540

ggtggttgga gtatcatgaa ctctgcagaa ggcggtcctg cgtttcaggt ggcggtatca 600

ttggctgcgt gcgtatattt tctgaatgag aagacaaaga gcttggggag agcttgctta 660

atcggaattg gagctttagt tgccgggtgg ttctgcggtt cgttaatcat tcccatgatt 720

ccgacgtttc tcattcagcc tacatggaca ctcgagctcc taacatcact ggtcgcttat 780

gtgtttttgt ttctttcttg tactttcctc aagtaagtta cgttgtggtt ttatccaaac 840

tctttttgtt cttttcgccc agacatttac agaacctttc ggaaaaatta gtgaaagttg 900

ttaagtgaaa aaaaaaaaaa aagggcggcc gcaccctagg ccagt 945

<210> SEQ ID NO 5
<211> LENGTH: 934
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

ctcaatggag tacaaacatt tcagccatcc acacactcta aaactccaac agattcagcc 60

acataaaagc tcagattctt cagtaatctg ctcaggttgt gaatcagcca tctctgaatc 120

cgaaaccgcg tatatctgtt caacatgtga cttcaatctt catgagcaat gtggtaacgc 180

agtgcgtggg atgcaacatc cttctcacgc tggtctccac cacttgactc tagtccctta 240

cacaacttac agcgctggta ccttcctctg cagagcctgt ggctgcactg gaggtaaagg 300

gttctcttac tgttgtcctt tgtgtgactt tgaccttcat gttcaatgcg ctcacctgcc 360

-continued

tcaggtcttg gttcatgagt ctcatcctat gcatagtctt cttcttgtct acaacagtac 420

tcctcctatg tcttttactc agtttggttt cgggaatcag cttgtttgca atctttgtaa 480

tatgactatg gatggtaggt tttggtctta caactgttat gcttgtaact atcatattca 540

tgcttcatgt gctgtgaata agcccaatcc agtggctgct tctgctgaga actgtggggc 600

gagtgatgaa ggaaagacac cgactgctga atctgttcct gttcagggtt tggagactga 660

gcagacggaa caagtagctg caataacaga gcaagtggaa gatccagttt tgaggcaaca 720

gcttgagctt cagaagcttc agcttgagct agatatgagt tctgctctcg caaacatgat 780

tggttccttc aatctcagtt ctttcgtttg aagtgtcttt gtgtttcagt ttgtttgatt 840

ttatgcattt acatgtgttg aattgtctct gttcttgtgt tccctaatgt gcttctgatt 900

tgaataaata tatcctatct atttggttta aaaa 934

<210> SEQ ID NO 6
<211> LENGTH: 761
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 6

aaaggatttg ctctgagggc tgggctcggg ggtcccagtt ccgaacccgt cggctgtcag 60

cggactgctc gagctgcttc cgcggcgaga gcgggtcgcc gcgtgccggc cgggggacgg 120

actgggaacg gctctctcgg gagctttccc cgggcgtcga acagtcagct cagaactggt 180

acggacaagg ggaatccgac tgtttaatta aaacaaagca ttgcgatggt ccctgcggat 240

gctaacgcaa tgtgatttct gcccagtgct ctgaatgtca aagtgaagaa attcaaccaa 300

gcgcgggtaa acggcgggag taactatgac tctcttaagg tagccaaatg cctcgtcatc 360

taattagtga cgcgcatgaa tggattaacg agattcccac tgtccctgtc tactatccag 420

cgaaaccaca gccaagggaa cgggcttggc agaatcagcg gggaaagaag accctgttga 480

gcttgactct agtccgactt tgtgaaatga cttgagaggt gtaggataag tgggagcttc 540

ggcgcaagtg aaataccact acttttaacg ttattttact tactccgtga atcggaggcg 600

gggtacaacc cctgtttttg gtcccaaggc tcgcttcggc gggtcgatcc gggcggagga 660

cattgtcagg tggggagttt ggctggggcg gcacatctgt taaaagataa cgcaggtgtc 720

ctaagatgag ctcaacgaga acagaaatct cgtgtggaac a 761

<210> SEQ ID NO 7
<211> LENGTH: 727
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 7

ctctttcctt ctctcaccgc gagagtaacc gagagacatg attctgataa actctaattc 60

tccgacgcta atctcagccg ttagattcgt gggctcatct ccgttcacca ctcgggggct 120

ttctcagtcc actgtctcaa tctctagaaa caaaagcttc ttcttccact tcaccgagac 180

gaaggagaag aacgcaagaa gagattattt gagagtatca atcgtgtgtg acgcaggagg 240

gatgtttccg gtggatccat gggctccaac cattgattca cagagcatag catcacaact 300

cttcgctgta tctctgtttc cttacattgg ctttctctat ttcctcacta aatccaaatc 360

agctccaaaa ctcacacttt tcggtttcta cttcttgctt gccttcgttg gagctacaat 420

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tccagctggg atttatgcta aggtgcatta tggaacatcg ttgtcgaatg ttgattggtt 480

acacggagga gctgaatcac ttcttgctct taccaatttg tttatcgtgt tgggtcttag 540

acaagctctg aggaagtctc aagatgatga tgatgataaa cttggtaatg atgatgaagt 600

tccaacaact caagaacaag ggaaatcttc agtgtagtaa aacaaatgta aatttttaa 660

ttatggagtt tcacttgttt tttaattaga ttatatatag tcgacgccca tctaattccc 720

attttag 727

<210> SEQ ID NO 8
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 8

tgactgatta ctactacttg tactaactct aatacattta caaaacaagt cctccttttc 60

cccaagtata cagataaaga tttaccagaa ccggttttcc gccttcatct cacatggaaa 120

tcgtaaggag aagacgcata cacttgatct ggaaccacta gtggtaactt ctcaatgtac 180

ataaacaatc gtttctggtt ctctctagcg attgcagtga gattcactgt atcgttttgg 240

tccaaaaaca tccagagatc acctgaatct actcttttaa ggctgtct 288

<210> SEQ ID NO 9
<211> LENGTH: 452
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 9

acctccagcc ctgatgatgg tgtatggaat accggaatca gccaagtatt gctcagcctt 60

tctcttccag accagaatgt tagcattgcc aatactattg agagggtgat taatgtttgt 120

tcctcccatc gacccaacca aaacaatctg cttaactcct gcagagacag ccttaaaaga 180

gtagattcag gtgatctctg gatgtttttg gaccaaaacg atacagtgaa tctcactgca 240

atcgctagag agaaccagaa acgattgttt atgtacattg agaagttacc actagtggtt 300

ccagatcaag tgtatgcgtc ttctccttac gatttccatg tgagatgaag gcggaaaacc 360

ggttctggta aatctttatc tgtatacttg gggaaaagga ggacttgttt tgtaaatgta 420

ttagagttag tacaagtagt agtaatcagt ca 452

<210> SEQ ID NO 10
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 10

aaaagccctc catgtcccac caggacttgc accatcaaaa tgggatactt gcagtgatgt 60

cgtgagtgaa cactggaatg actctccttc ctcggttcta aacatttacc acgagcttat 120

agctgctggg cttcgtatct gggttttcag tggggacgca gatgccgttg taccagtcac 180

atcaacccgg tacagtatcg atgcactaaa ccttcgtcct ttgagtgcct atggtccttg 240

gtacttagat ggacaggtgg gagggtggag tcagcagtat gctggtctga actttgtgac 300

agtgagaggt gcaggccatg aagttccttt gcacagaccg aagcaagctc ttgcgctctt 360

caaggctttt atatctggaa ctccattgtc cacacatgag aacagcatca gccgcgacat 420

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gtctgaactc gttagtgact cataatgagt tctgatttga tgtaatgtgt gatttggatt 480

ctcaatcaaa aactttccac ataggccgtt gaaataagaa gagggaaaga gaataaatca 540

gtgttttaag tg 552

<210> SEQ ID NO 11
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 11

ttttgaatga ataaaagtct tataattatg atgtgtgtac aactacaaag ttttccttgg 60

agtatagttt gaggatttat ccagaagtag cagaagaagc agctacagac tcggagagtt 120

cttccatgag ttccttttgc tccaaagcag cacaagcctg cactgcgtcc tctaaagcac 180

cgtcaagaaa tgttgtaagc gcaaagttca tctttagcct atgatcagtc actctactgt 240

ccttataatt gtatgttctt atcttttctg aacgagctcc agtcccaacc tgagatttcc 300

tttcattcct tatcttctct tgttgttccc ttacttttat ttcatacagt tttgctcgca 360

gaagctggaa agcacgcgcc ttattcctaa t 391

<210> SEQ ID NO 12
<211> LENGTH: 200
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 12

ctgcagctgt gtgctcctta gctaaggtgg caatggcaga cgatgagcca aagagaggaa 60

cagaagctgc caagaagaag tatgctccag tctgtgtcac aatgcctacc gccaagatat 120

gccgtaactg agtttgctat ttaaccagca actgtatcta tgtcgtataa ctattctcag 180

tgtggtttgt aaggatcata 200

<210> SEQ ID NO 13
<211> LENGTH: 1063
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 13

ttttccagtc tgcaacatat ggaaaggttt tggttttgga tggagtgatt caactcactg 60

agagagatga atgtgcgtat caagaaatga tcactcatct tcctttgtgc tctatctcca 120

accccaaaaa ggtactggtg attggaggag gagatggagg agtcctgagg gaagtggcac 180

gtcatagttc tgttgagcag attgacattt gtgaaataga taaaatggtg gttgatgtgg 240

ctaagcagta tttccctaat gtagcagttg gatacgagga tcctcgtgtc aacctcatca 300

ttggcgatgg tgttgctttc ttgaagaacg ctgctgaagg aacctatgat gcagttattg 360

ttgattcatc tgatccaatc ggtccagcaa aagagctatt tgagaaacct ttctttgagt 420

cagtgaatag agctcttcgt cctggtggag ttgtgtgcac acaagctgaa agcttgtggc 480

ttcacatgga tatcattgaa gacattgttt ctaattgccg tgacatcttt aaaggatctg 540

ttaactacgc tggttctctg agattagtcc tatgtggcca ggagaagcac attctctcaa 600

ggtagagaag attctattcc aagggaaatc agattaccag gatgttattg ttggaccagt 660

gttccaactt acccgagtgg agtcattgga ttcatgcttt gttcatctga aggaccacaa 720

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gtcgatttca agaagccagt gagtctaatc gatactgatg aaagctctat caaatcacac 780

tgtcccttga agtattacaa cgctgagatt cactcagctg ctttctgctt gccctctttt 840

gctaagaagg tgattgattc gaaagccaac tagaaaagag aagagaaatc atttgcttta 900

gagaaacttc atgtggaagt gataatatga tgatacaatg atcctttgga aaaaaataaa 960

gaagttttaa tttttagaat gtaatgttct ttcacctgca atgttatgtg actgcactga 1020

gctatcaatc tctttttata agcattacac atatttcaaa aaa 1063

<210> SEQ ID NO 14
<211> LENGTH: 1173
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 14

aaatccccaa attttcaaca aggataagag ccggaagctc atcgccggtg aacggaacta 60

gggtttcatt catccccaaa ttgataacaa gaaaatggct catgcttgcg tctctacatc 120

ggcttcttct ctcagattca cagctggatt cgtctccgct agtcccaatg gctcctcttt 180

cgattctccc aagctttctc ttcctttcga gcctctccgt tcaaggaaga cgaataagtt 240

agttagcgat agaaagaatt ggaagaattc aactccgaaa gctgtatatt ccggcaatct 300

ctggacaccg gagattccgt ctcctcaagg agtttggtcc attagagatg atttacaagt 360

cccttcttcg ccgtattttc ctgcttatgc tcaaggacaa ggaccacctc ctatggtgca 420

agaacgtttc cagagtatca ttagtcagct cttccaatat aggattattc gctgtggtgg 480

tgctgtggat gacgatatgg caaacataat tgtagctcaa ctcctgtatc ttgatgctgt 540

tgatcctact aaggatattg tcatgtatgt taattctcct ggtggatcag ttacagctgg 600

catggctata ttcgatacta tgaggcacat ccggcctgat gtgtccactg tttgtgttgg 660

tctagctgct agtatgggag cttttctgct tagtgctgga accaaaggaa aaagatacag 720

tctaccaaac tcaaggataa tgatccatca gccgcttggt ggagctcaag gtggccaaac 780

cgacattgac attcaggcaa atgaaatgct gcatcacaag gcaaacctaa acggttacct 840

cgcataccac actggtcaaa gcctggagaa gataaaccag gacacagacc gtgatttctt 900

catgagtgcc aaagaagcaa aagagtatgg acttatcgac ggtgttatca tgaaccctct 960

taaagctctc cagccacttg cagcagctta atcgcctaaa ggtagtggtt cagctttagc 1020

acttgttctt ttttgggcct ttgatgaact gagattttcc atgaaatatg tttctattct 1080

acaaggaaaa tcagatttgt ttgggatcaa actctgtagt tgatacatac atgaagacca 1140

aagtaaagtt tcttactgtg ctgaaaaaaa aaa 1173

<210> SEQ ID NO 15
<211> LENGTH: 959
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 15

agaaacgatg agttctcaga tttcggagat tgaacaagag cagctgatcg agaagcttga 60

gatcttcaag atccatggca gagacaaacg tggccgtaag atccttcgta ttatcggaaa 120

attcttccca gctcgatttc tgtcactgga tgtgttgaag aagtatctag aggagaagat 180

atttcctcga ttaggtagaa aaccattcgc cgtactctac gtccacaccg gcgtacagag 240

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aagcgagaac ttcccaggta tctcagctct acgagcgatc tacgacgcaa ttccggtaaa 300

cgtcagagac aatcttcagg aggtttactt cctccatcca ggtcttcaat cacgtctctt 360

cctcgccacc tgcggccgat ttctattttc cggcgggttg tacgggaagc tgaggtacat 420

aagcagagtt gattatctgt gggaacatgt gaggaggaat gagatagaga tgccggagtt 480

tgtatacgat cacgatgatg atctggagta tcgtccgatg atggattacg gtcaagaaag 540

cgatcacgcg agggttttcg ccggagccgc cgtggattca tcagtctcaa gtttctccat 600

gaggtgtatc tcatagcgta aaaggctaaa actccaccca ctagatatcg gatcgtatct 660

tataaaccat ataatatacg aatacgatta ataatatatc aaaaagattg gaaataggtg 720

tgctttttga aattagtgag cgtttttttat ggaaaagaaa agaaaagaaa gcagttggcg 780

tctggataaa gggaaggagg agaatcttta gatttttct ttaatctgtt tttcttttgt 840

cttgattagt tttttcttta gtggtggtgg ttgtgagtta gtgtgtaaaa tgtatattgt 900

catatgtgaa tttaataata agtccttttg taagatgatc aagggaaaaa aaaaaaaaa 959

<210> SEQ ID NO 16
<211> LENGTH: 250
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 16

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gacagactta tgatctcata cctatctatc ttccatcact ttcatgtctg tctgtgagtg 120

tgtttcatct tagagttctt ggtttttgag cttgaattat tgttgaaccg ttgtagctcc 180

atgaacaaat ttggaatctt caatgtacag aggaactaag ttaatcaaca ttgttgtact 240

ctttaaaaaa 250

<210> SEQ ID NO 17
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 17

ttttgaatga ataaaagtct tataattatg atgtgtgtac aactacaaag ttttccttgg 60

agtatagttt gaggatttat ccagaagtag cagaagaagc agctacagac tcggagagtt 120

cttccatgag ttccttttgc tccaaagcag cacaagcctg cactgcgtcc tctaaagcac 180

cgtcaagaaa tgttgtaagc gcaaagttca tctttagcct atgatcagtc actctactgt 240

ccttataatt gtatgttctt atcttttctg aacgagctcc agtcccaacc tgagatttcc 300

tttcattcct tatcttctct tgttgttccc ttacttttat ttcatacagt tttgctcgca 360

gaagctggaa agcacgcgcc ttattcctaa t 391

<210> SEQ ID NO 18
<211> LENGTH: 1004
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 18

agaactagtc agtttctttg ttttagacaa caagaatctg tgaactaaca caaaaacatt 60

gaaagaatga tcttaacaat gaaacttgtt caccctctcc atcactcttt gtcttcctcc 120

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attccctttc cctcaagaaa aaggcaatcc aaaccgtacc ggtgctcgtt accttctccc 180

ggctgcgaaa aggtcatcag aacagagact gtcctgcctc cggcgccggt gagttgtgaa 240

gggagaaggg tcttacttgg atgtcttctc gctacagctt ctgggatttt gtcaactggt 300

tcagccgagg cagtaagcac cagtagaaga gctctacgtg catccaagtt accggaaagc 360

gatttcacga ctctccccaa tggtctcaag tactatgata taaaggttgg caatggagca 420

gaggctgtga aaggatctcg ggtcgcagtt cactatgttg caaaatggaa agggataacg 480

ttcatgacaa gtcgacaagg acttggtgtt ggaggtggaa cgccttatgg gtttgacgtt 540

ggtcaatcag agagaggcaa tgttctgaaa ggacttgatc ttggtgttga agggatgcgt 600

gtaggcggtc agagattggt gattgttcct cccgagctgg cttacgggaa gaaaggagtg 660

caagagattc ctccaaacgc tacgatagag cttgacattg agctgttatc aatcaagcag 720

agtcctttcg ggacgccagt gaagatagtt gaaggctaaa aggactaatg aagccaacat 780

tgtaccaaga ttttctgtgt acattcagta aaaaactata aaattgatca aagctatgga 840

agattcaact gtatgagaag aatctgttta atggattata ccggctagtc cggttttgta 900

accgctttat aactgtgtct catcactcaa ttcatacact tttggccgtt ttgcaaaaaa 960

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1004

<210> SEQ ID NO 19
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 19

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actcttctca tgacaaatcc aggtcgaagc ggtcaaggtc cagatcaaga tccccccaca 120

ggcgccatcg taaatgaaca ctctagcaaa ctggtctgag actgtacccg ggacaatatt 180

gtgcgcggtg gatcacagga ttgggttaat gtactggacg gacatcgata taatcaaaaa 240

ctataaagtc accggtttgt gagcgaaata gtgcatagta aaccgctctt tccttagttc 300

ttcagaagaa atatccaaag atttttgact gacttgtttg acaatatcgt tggttggtta 360

agcgttccta tgtaaaattt tgttccctct gaaaaaa 397

<210> SEQ ID NO 20
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 20

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atacataata gagagataaa agacatcaaa cataaccaac atgaaatcaa ctagaactca 120

aaacaagacc agacttaaac atcatcaatt agttgatttt actttaaatt catttaaaca 180

taaaaagcaa agaagaaact tcttaaaaga agaatccaaa ggccatcacc gctacggagg 240

cgaagaaagt agggataaat gaggaagcat cggaggtagg gctaggcgcg ggagcgtcaa 300

ccgctgcaac cgtctggtga actgtagaga acgctatcac tgccaccaaa accgccacga 360

aaagcttcat cttcattgcc tccattgtta gtaaatgaag agaagaaaag aggttttggt 420

gcttactgtt gtgttgttgg tt 442

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<210> SEQ ID NO 21
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 21

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taatgataat gggagaaaga aatccctaaa aaaaaattga aaatgggaga aagaaaacca 120

agaaggtttt gtttcatctc ctttcttccc ataagccttt ttcttgtatt gttcccttct 180

cttctctaaa taaaaaaaaa aaaaactgtt ttttgtgaaa attaattgac caaaaacaaa 240

gaaatcttct ttcttctctt ctcttctttg ttaatcttgt tacccttcta ccaccaccac 300

ctgtaaaaaa gaggttttta tctaccacat agagagacca gacaagaaca tgtgattctt 360

tggttaggtc tctcaattct gctgagccac aagctgatcg agctgcattt gctcaatcca 420

agcttctagc ccagcatgat ccattaccgg ttcaaccgga tttggctgct tcatcacgtg 480

ttcccctgag gaagatgttg ctgctttctc tttggcttct gctggagtct ccttcaccag 540

tgactggacc catgacacat caggctcatc accatcaaac gatgacgaag atctcaactt 600

accaagtgct tctgagctca ttccccaatc cggttgacca tttgaagatc cccattttga 660

tgaccatgtg ttgttgttta ccggtgaacc aacgattggg ctagagtttg ttctgagctc 720

tctggagcta aggctacgga actgatgttg ctgctgctgc tgctgctgtt gctgttgttg 780

ttgcttcacg cactgagcca acatggaaac ccg 813

<210> SEQ ID NO 22
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 22

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actcttctca tgacaaatcc aggtcgaagc ggtcaaggtc cagatcaaga tccccccaca 120

ggcgccatcg taaatgaaca ctctagcaaa ctggtctgag actgtacccg ggacaatatt 180

gtgcgcggtg gatcacagga ttgggttaat gtactggacg gacatcgata taatcaaaaa 240

ctataaagtc accggtttgt gagcgaaata gtgcatagta aaccgctctt tccttagttc 300

ttcagaagaa atatccaaag atttttgact gacttgtttg acaatatcgt tggttggtta 360

agcgttccta tgtaaaattt tgttccctct gaaaaaa 397

<210> SEQ ID NO 23
<211> LENGTH: 625
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 23

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atagaagaat attgattcgg taacaaagca cagcttataa gttttcttgt gttaaagatg 120

aaccaatttg aagcattaga ggataaactg gactaaactc tttgtcccct ctcgatctga 180

tcttcactgc ataatcatcc aaagttgctt ttatcccttt ccagatctga tcctctcttt 240

ggttatcaag ccacagtgag tactgtttag gacttagtct gttcttctgc atcggtgact 300

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ctaactcgtc tgggcctctt gtgtagagat gatgtaggac gatgctcggt ggtagatcat 360

tgatgagagg agatgatccc atttgagatg tttccaggaa aaccaaaggc ctaaacgctc 420

taagagctct gtacggtgct ccgagttgtt ccacgggaaa tagattctgt cccactgcta 480

gttccagctc ggccatgtct ttggccattc tgagttttcc ccattctgaa agtggtcgca 540

caagggatgc atgtctgatg tagaagatca aaaccttga cgccatttgt cttgtgagtc 600

ttgtgcagat cgattctgtt cctgc 625

<210> SEQ ID NO 24
<211> LENGTH: 959
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 24

agaaacgatg agttctcaga tttcggagat tgaacaagag cagctgatcg agaagcttga 60

gatcttcaag atccatggca gagacaaacg tggccgtaag atccttcgta ttatcggaaa 120

attcttccca gctcgatttc tgtcactgga tgtgttgaag aagtatctag aggagaagat 180

atttcctcga ttaggtagaa aaccattcgc cgtactctac gtccacaccg gcgtacagag 240

aagcgagaac ttcccaggta tctcagctct acgagcgatc tacgacgcaa ttccggtaaa 300

cgtcagagac aatcttcagg aggtttactt cctccatcca ggtcttcaat cacgtctctt 360

cctcgccacc tgcggccgat ttctattttc cggcgggttg tacgggaagc tgaggtacat 420

aagcagagtt gattatctgt gggaacatgt gaggaggaat gagatagaga tgccggagtt 480

tgtatacgat cacgatgatg atctggagta tcgtccgatg atggattacg gtcaagaaag 540

cgatcacgcg agggttttcg ccggagccgc cgtggattca tcagtctcaa gtttctccat 600

gaggtgtatc tcatagcgta aaaggctaaa actccaccca ctagatatcg gatcgtatct 660

tataaaccat ataatatacg aatacgatta ataatatatc aaaaagattg gaaataggtg 720

tgctttttga aattagtgag cgtttttttat ggaaaagaaa agaaaagaaa gcagttggcg 780

tctggataaa gggaaggagg agaatcttta gatttttct ttaatctgtt tttcttttgt 840

cttgattagt tttttcttta gtggtggtgg ttgtgagtta gtgtgtaaaa tgtatattgt 900

catatgtgaa tttaataata agtccttttg taagatgatc aaggggaaaa aaaaaaaaa 959

<210> SEQ ID NO 25
<211> LENGTH: 618
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 25

ctttcatgtg agagagagag ttgaattttg cagatgagta tgagaagaag caaagcggaa 60

gggaagagga gcttacgaga actgagtgag gaagaggaag aagaagaaga aactgaagat 120

gaagatactt ttgaagaaga agaggctttg gagaagaagc agaaaggtaa agctacaagt 180

agtagtggag tttgtcaggt cgagagttgt accgcggata tgagcaaagc caaacagtac 240

cacaaacgac acaaagtctg ccagtttcat gccaaagctc ctcatgttcg gatctctggt 300

cttcaccaac gtttctgcca acaatgcagc aggtttcacg cgctcagtga gtttgatgaa 360

gccaagcgga gttgcaggag acgcttagct ggacacaacg agagaaggcg gaaaagcaca 420

actgactaaa gacggtgaaa cgtgtgagat cccggtttga aggttaatga aacaggcttt 480

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gcttactctc ttctgtcagt ctcttttagc tccttgtaat cctctgtgtc tctgtctgtt 540

tctccatatt acctgtaatc aaagctatct gctaaaccta cgacatggtt aaataaatgc 600

attgagactt agtaaaaa 618

<210> SEQ ID NO 26
<211> LENGTH: 1094
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 26

atcttatgca agaagttgct gtggagacat ttggtgctat ggcaaaaact gagaaaattg 60

catttatcct tgaacaagtt cgcttgtgct tggatcgtca agattttgtt cgtgcacaaa 120

tcttatctag gaagatcaat cctagagttt ttgacgcaga tacaaaaaaa gataagaaga 180

aacctaagga aggtgataac atggtagaag aggctcctgc tgatatacca acccttttgg 240

agcttaagcg aatttactac gagcttatga ttcggtacta ttctcataac aatgagtaca 300

ttgaaatctg ccgtagctac aaggcgatat atgatatccc ttcagtaaaa gaaactccgg 360

agcagtggat tccggtcctg aggaagatct gctggttctt ggtcttggca cctcatgacc 420

caatgcaatc aagcttgctc aatgcaactc tggaagacaa gaatttatca gaaatccctg 480

atttcaagat gcttctaaaa caggtagtga caatggaggt tattcaatgg acatctctgt 540

ggaacaaata caaggatgag ttcgagaaag agaaaagcat gattggaggt tctttgggtg 600

acaaagctgg tgaagatctg aaactgagaa tcatcgaaca taatatcctc gttgtctcaa 660

agtactacgc aaggataacc ttaaagagac ttgccgagct tttatgcctg agcatggagg 720

aggcggagaa gcatctatcg gagatggtag tgtcaaaagc actgattgca aaaatagaca 780

gaccatctgg aattgtgtgc ttccagatcg caaaggacag caacgagatt ctaaactcgt 840

gggcagggaa tttggagaag cttctagatc ttgtggaaaa gagttgccac caaattcaca 900

aggaaaccat ggttcacaaa gccgctctca gaccttgaaa acatgcggtc ttcttcatga 960

aaacttttca ggatcttctt cgttgagtta ttagcatctt tatgtggtaa aaactcgaat 1020

cagtgtttcc ttttaaaaat tgtactatgg atctgtacac taacgaagtg ttttgccact 1080

tattggttaa aaaa 1094

<210> SEQ ID NO 27
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 27

ttttgaaaca taaacaaaac tcttatttat taaggacttg tgctaaatac atttagcctc 60

aaacatccaa aacttacatt ttcataaaag acacgatgag gtgtggtgtt aacatgtatc 120

aacaaccaca ctctcatacg ctcgagggtt tttgtttgga atctattagt aaggagggaa 180

gaaagggatg gtggtctgga aggggcattc accaacttgc tggatcttgc aaatgttagg 240

caagtactta gctgtcttgt aaattttcct ggattggaat ggtccgtgtt gtccctggag 300

gctaacggcc ctggcagctt gtctcaaggt ggggcaaaca caaactggct cttcctggcg 360

aagctcg 367

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<210> SEQ ID NO 28
<211> LENGTH: 949
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 28

ctaatggaaa taccgaggcg aatgtagtgg aagctgtaga gaatgtaaag aaggataaga 60

agaagaagaa gaacaaggaa acaaaggtgg aggtaactga ggaagagaag gtcaaagaga 120

ctgatgctgt gattgaagat ggagttaagg agaagaagaa gaagaaggaa actaaggtga 180

aagtaaccga ggaggagaag gtcaaagaga ctgatgctgt gattgaagat ggagttaagg 240

agaaaaagaa gaagaagagc aagtcgaaat ctgttgaggc tgatgatgat aaggagaaag 300

tttcaaagaa aaggaaaaga tcagagcctg aagagactaa agaagagact gaggatgatg 360

atgaagaatc aaaacgtagg aagaaggaag agaatgtagt tgaaaacgat gagggtgttc 420

aagagacacc tgttaaggag actgaaacta aggaaaacgg aaatgctgag aaaagtgaga 480

caaagtcaac aaatcagaag tcaggaaaag ggctttctaa ctcaaaagag ccgaagaaac 540

cgtttcagag ggtgaacgtt gacgaaattg tgtacactga gaatagcaac tcgtactatt 600

caaagggtgg tgctgaaatt ggctatggtc ttaaagctca agaggttctc gggcaagtga 660

gaggaaggga tttccgacat gagaagacga agaagaaacg aggaagctac agaggaggat 720

tgatcgatca agagtcacat tcgactaagt ttaataactc agacgacgaa gaatgattga 780

taagcagaca acactgcctt tttgacattg cttcgtttcg atttatcttt ttcttttctt 840

ttgctttgat catttcaata cccgtaatag ggctcaagtt ttgtgtctgt gcactccttt 900

gatacttata tgaacatgat tcagtttcag tttcttgttc aaaaaaaaa 949

<210> SEQ ID NO 29
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 29

ttttttttt ctctcgcaaa cagaaattta tattgacttt taagaacaaa tacaaagtat 60

atctatcaca caactcacaa aagagatagg tacaaacata atgacaaatc acaatcagca 120

caccattaca ttaaaagtca aatttacctt tttaataaga agatacaaaa atatataaag 180

agaagaccaa gacaatttga cttgagtgat taggaggcat tgttggcctg taataatcca 240

tttcgaatct gcgttgccac gtcagcgacg gcgcctggac cgtgagggat aaacaccgcc 300

gaggctttag aagttgctcc gatatctctc attgtgtcaa agtactgagt catcatcacc 360

atgtccaaca catccttcgc tgacgtccct ggcacgtttc ctgcgaaccc tagaacactg 420

tctctcagac cgtccacgat cgcttgtctc tgccgagcga ttccgagtcc cgacaggtac 480

tttgactctg cttcaccctc tgctcttttg atctgaatga ttttctcagc ctctgctttt 540

tcgctcgctg ccactctcat cctcgccgcg gcgttgattt cgttcatggc acgtttaacc 600

tgttgatcag gctcaatgtc gataattagg gtttgaagga tttcgtaacc ataagcagtc 660

atggctttgt ctagctcttc ttccacagat ttggcaattt cattcttctg c 711

<210> SEQ ID NO 30
<211> LENGTH: 1132
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 30

gaacatcaga aaaaggcatg taatattaat tcagccaaca tctgtggata tgcaggtgtt 60

gaagagaaac ggtacaaatt aaagttgatt tcttttactt tgttacagct acgtaccata 120

caatcaccca aacatacaaa accttaaaag acaaaagttg gcatctctat cagttgggtt 180

ctagtcaatc ttcactgagg agtagatctt tctcacgaac cagaagcaag catagaaacc 240

gattgtgcca gttaggacga agaatgcgta agagatgata atcatgtacc cgaagtagag 300

cattcccgag actagctttg tgatctccag ctttgtgaag aagtagaaga ttgagtagag 360

gaagaggtag aaagcggatg agcccgcagt taagtaagct ctccaccacc agttgtagtc 420

ttcgctacaa agctggaagt agcagagcac cactgtgatc tctgcacagg tgacgatcaa 480

gatcaaaaaa actataaaga ggaacccgaa gatgtagtag aactggttca gccatataga 540

tgtcaagatg aagaagagct cgatgaagac tgctccaaac gggagaatgc ctccaattag 600

tatagagaaa actggtttca tgtaccacgg ctgctctggt acttgcctcg ggatcttgtt 660

tgttttgact ggatcttcaa ttgctggctt cttgtaaccc agatagctac caacgaagac 720

tagtgggact gagatgccaa accagaggca gaagagagca aacattgtac caaatggtat 780

ggctccagat gactgttctc cccaaataag ggcattcaga acaaagaaga tagcaaaaag 840

gataccggga aacatgaatg cagtcttcaa ggtcattctc ttccacttgt ttcctttgaa 900

cattttgtga aggcgagacg aggagtaacc agcgaatatg cccatgaaaa cccacaagag 960

aaccatggca gtcataagcc ctcctctgtt ggatggagat aagaagccaa gcaacgcaaa 1020

catcattgta acaagtgaca ttccgaagat ctgaacacct gtaccaacat aaacacacaa 1080

taaaccagag ttcaccggtg gcctgaagac atctccgtgt acaagcttcc at 1132

<210> SEQ ID NO 31
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 31

agtgaagcaa tggagtccag atggagtgac tcggattggt gtgattggga aatcggtata 60

ttccgtgaaa ttctccggta tatctacccg gaagatgctc caccaaccgt cgtctgcttg 120

cggacgcgtg ggtcgacccg ggaattccgg accggtacct gcagaggaag atgaagattt 180

aagttgggac attgatgaag atgacgaaga agaatcatca tcatccaaag cttaatgtta 240

gttttaaagt ggtgtgcttt cttacttttg ccaatccttt tacttgtttt tacaagtttc 300

tggcgctttg cccccattct tcagttgttt ctctcttcaa cgtttctatt ttacattgat 360

ttgaaaatat gtttttaaat tttaaaaaa 389

<210> SEQ ID NO 32
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 32

gaagaagaag aagtaatggc ttcctctatg ctctcctctg ccgctgtggt tacctccccg 60

gctcaagcca ccatggtcgc tccattcact ggtttgaagt catccgcttc tttcccggtc 120

acccgcaagg ccaacaacga cattacttcc atcacaagca atgggggaag agttagctgc 180

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atgaaggtgt ggccaccaat cggaaagaag aagtttgaga ctctatctta cctccctgac 240

cttactgacg tcgaattggc taaggaagtt gactaccttc tccgcaacaa gtggattcct 300

tgtgttgaat tcgagttgga gcacggattt gtgtaccgtg agcacggaaa cactcccgga 360

tactacgatg gacggtactg gacaatgtgg aagcttccat tgttcggatg caccgactct 420

gctcaagtat tgaaggaagt tgaagaatgc aagaaggagt acccgggcgc cttcattagg 480

atcatcggat tcgacaacac ccgtcaagtc cagtgcatca gtttcattgc ctacaagccc 540

ccaagcttca ctgatgctta aatccttttc tggaatattc aatgttgact atccggaacc 600

caattttgta tggtcaatgt aaatttaagt aattattttg ccaaagtgaa aaaactgaag 660

gtttgttttt ctatcatttc ctctataaaa atctctattc atatcacttc a 711

<210> SEQ ID NO 33
<211> LENGTH: 607
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 33

agcaaccttt ctctgaattc ggggaaatag tgtctgtcaa gattcctgtt ggtaaaggat 60

gcggatttgt tcagtttgtt aacagaccaa atgcagagga ggctttggaa aaactcaatg 120

ggactgtaat tggcaaacaa acagtccggc tttcttgggg ccgtaatcca gccaataagc 180

agcctagaga taagtatgga aaccaatggg ttgatccgta ctatggagga cagttttaca 240

atgggtatgg atacatggta cctcaacctg acccgagaat gtatcctgct gcaccttact 300

atccaatgta cggtggtcat cagcaacaag ttagctgagg aaactaaaag cttaatctga 360

gcatctatct ataggacaac aaaaactcac tcaggttagg tgatgttagg aggtataagg 420

caaaagtggt tggcttcttg tctctacttg agtttagggt ttatcatctt ttggacatcg 480

aattttggtg gaaatcatac agtaatttag gagacttgga tttgattgat taatttgatt 540

tgtttcttct gatctttttg actattgaac ttattgatca aagaagtgag ttgcaccaaa 600

aaaaaaa 607

<210> SEQ ID NO 34
<211> LENGTH: 874
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 34

gtacaatgtc tcctatgtct accatgccct agatgcctac atcgagagag acaatgtcgg 60

cttgaaaggt ttcaccaagt cagtttcttt agtctaaagg aaaaccgtat ttgtgtctct 120

tcagctggtg gatcatcttt ttgttattgt tgagggttta acgctaatag gttctttaac 180

gattcaagtc ttgaagaacg aggttatgct gagaagttta tggagtatca gatgcattgt 240

ttgcgatgga gcttgcactg actttggaga aacttattaa tgaaaagctt ctgaagttac 300

aaagtgttgg tgtgaagaac aatgatgtta agctggttga ttttgtagaa tctgagtttc 360

taggcgagct ggtcgaagcc atcaagaaaa tctcagagta catagatgga acaaaaataa 420

ggtcaatgca gtggtgaagc tgagatcgga tgtttctgat ataagctggc aagtgaagat 480

ggagggtcaa agactaaccc aaggctggca aaagttcgca acaagccacg atctccgagt 540

cgtcgacata gttgttttca gacatgatgg agatttcttc tcaaaacttt gaattctttg 600

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aattctttgt ttcgagatct atcgatactc gacatcaaag aactccttat aactcttgat 660

tcattgaaac aagagtaggc atgtcaatcg agctatcccg gtccgacccg aaacccgtaa 720

tacccgtata tgtttgagtt tgggtcagaa aagctctgag cctatatttt aatttaggta 780

tttcctgtat tttttatttt ttgtattcaa tttctccaaa attagtggaa attatccata 840

ttttctttct atttttttaa aaaaaaaaaa aaaa 874

<210> SEQ ID NO 35
<211> LENGTH: 874
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 35

gtacaatgtc tcctatgtct accatgccct agatgcctac atcgagagag acaatgtcgg 60

cttgaaaggt ttcaccaagt cagtttcttt agtctaaagg aaaaccgtat ttgtgtctct 120

tcagctggtg gatcatcttt ttgttattgt tgagggttta acgctaatag gttctttaac 180

gattcaagtc ttgaagaacg aggttatgct gagaagttta tggagtatca gatgcattgt 240

ttgcgatgga gcttgcactg actttggaga aacttattaa tgaaaagctt ctgaagttac 300

aaagtgttgg tgtgaagaac aatgatgtta agctggttga ttttgtagaa tctgagtttc 360

taggcgagct ggtcgaagcc atcaagaaaa tctcagagta catagatgga acaaaaataa 420

ggtcaatgca gtggtgaagc tgagatcgga tgtttctgat ataagctggc aagtgaagat 480

ggagggtcaa agactaaccc aaggctggca aaagttcgca acaagccacg atctccgagt 540

cgtcgacata gttgttttca gacatgatgg agatttcttc tcaaaacttt gaattctttg 600

aattctttgt ttcgagatct atcgatactc gacatcaaag aactccttat aactcttgat 660

tcattgaaac aagagtaggc atgtcaatcg agctatcccg gtccgacccg aaacccgtaa 720

tacccgtata tgtttgagtt tgggtcagaa aagctctgag cctatatttt aatttaggta 780

tttcctgtat tttttatttt ttgtattcaa tttctccaaa attagtggaa attatccata 840

ttttctttct atttttttaa aaaaaaaaaa aaaa 874

<210> SEQ ID NO 36
<211> LENGTH: 582
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 36

aaaagaagct tcatgtatct gatgaagatt ttgccaagtg gaagtttgcg ttcatgtcaa 60

tggggcgtcc agagtacttg caggacacag atgttgttta taatcgcttc cagagaagag 120

atgtctatgg tgcttttgag cagtacctcg ggttggagca tgctgacact actcctaaga 180

gggcttatgc tgcaaaccag aaccgccatg cttacgagaa gccggtaaaa atatacaatt 240

agccccaaaa catgaacaca aatgtcagga gacattgtgg cagcaacgtt ggaccaaggc 300

attgattgga ccaatgcatc gaataagaag ggaaagggcg agtgtgaggg tgtgatgatg 360

accgtaggat gttgtagaga atctggtctg atagggtttt gggttgcgca ttgatagtgg 420

tgtgttttct atttttttct tttcaatcta tccttatttt atttcgtgct tcaatacttt 480

gtgttaatat ctggaatgtg tgaagaccat tgcacatgca atttttattt tccaaaaaaa 540

gaatatggaa gcccttcgct tggaaaaaaa aaaaaaaaaa aa 582

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<210> SEQ ID NO 37
<211> LENGTH: 938
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 37

agttattaag cttttaaatt ttataaataa ttaattatta tcttaactaa tcttgatctt 60

ttttattttt tatttttttg gttagctgga aaataaattg tcggcaatta cagatcaaaa 120

tgaggcggag aaatatgtag atgtgattga cccaagggat attaagattg ggagcagaaa 180

attttataga tacattggat cacttactac tcctccttgt acgcaaaatg ttatttggac 240

cgtcgttaaa aaggtaaata ctcatcgtta ttttcttctc ttttttactt aatcaaacat 300

agcattaata gatcattaca aggtactaat agtgtgaata tccatatcca aaaggtttat 360

ccatctacat gttaactagg tctatttttc caattttaaa ttttgacttt ttattttaaa 420

atcattcgtt taaatttatt tggttggttt tttaggtaag gactgtgacg aaaaaccaag 480

tgaagctact cagagtggcg gttcacgatg taagttttac ttaaataatt tacttagtga 540

atttcacaac tatactatat cttagaagtt gaatgtatat tatatttgtt tattatcaaa 600

aatgtaaata tgattgaaaa ataaatttgc agaattcaga tacaaatgcg agaccagttc 660

aacctacaaa taagcgcgtg gtaaagttat acaaaccaaa atcactatga atcaaggcgt 720

cacatgaatc aaatacaatt aatttatttc aatttttttac aaccacagtg tactatttat 780

ttaatttttt tgttcaccaa agtttttata tataacacga aaaatatatg atgtatgtgt 840

tttcctgagt atcctatggt gtcccatctt cctcctgtag tttcaagatc ttcaatccaa 900

tctaattcaa atataaaaaa aaaaaaaaaa aaaaaaaa 938

<210> SEQ ID NO 38
<211> LENGTH: 1386
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 38

gattctctct ctagcgatgt cgatcaaacc ggagaattct ccgattccgt tgattgggat 60

taataatacg tgtgaaatca tggtgtcttt gagttcatga agaacggagg ttaacctaat 120

cgaagatttg atttgggact gcgaatgaga gagaagacgt tgaaggctca aattggagat 180

ttctatgaat ttgttgattt gagagaagaa ttgaggctca ttcgtaacgg agggaaggtg 240

acggtgacgg cgatggtgaa tttatagttg tacacggagc tggaactcat caaggacaaa 300

gaaggcaaag ctactcatct acttaagttc tgctccaaag ctgaaatacg gagattcaga 360

tcctttgttc ccatgaatca actacagacg ctttaataat ctgagggaat cttccgtgcc 420

aatatggaga gatcatcatc atcatcatca tcatcatcat caacatcatc atcatcatca 480

ttatcatcat catcatcatc gtcatcgtca tcgtcatcat catcgtcatg tgatcaggta 540

atattgactg gatcagcaaa ttcgccgacg aattagagtg gaacctcaga gggaattttt 600

tttttacgat ttgtctaatc tgattcgaaa ttttgtctcg tggtgatgcc gatgaaatag 660

aagatgtgta cctttcatat cattcactct ggttttatgg gatcagaaga aattagcgag 720

agtaaaatct gtggacctgc accatgtaac ttgattatgg cactcagtcc gagtaaggtt 780

ctgacacatg ttatctcatt ctatgtttac atgcttgttc atcttcaggt ttggaatctt 840

-continued

ggtttacctt acccaacttt tacattggcc attgacgata agccctatct aaataccgtc 900

tctgatgatc actctgttaa ggtcaaaaat gttgattgga tcagcaaact ccctgacgat 960

gtattgctca taatattatc gagactttcc acagaagaag ccataaggac gagtgttgtg 1020

tcgaagcgat gggaacatgt gtggagtcaa atgtctcatc tcgtcttgga catgcggaag 1080

aagattatca attccaacaa cacgcctgat ggttcgaatc cagttgctac attgattact 1140

caggttataa acaatcatcg tggacatcta gagagctgcg tgatcatgca tgtcccatat 1200

caaggtggaa atggaatgct caattcttgg attcgattac tgagttgcat gaaacgcacg 1260

aaagttctca cacttagaac cattatgata cttgggatcg aaagttcaaa acttttaact 1320

tttctcccga ctccttgtcc catccaagtc ttatgtcact ctcgctacat tcatactttc 1380

tcgaaa 1386

<210> SEQ ID NO 39
<211> LENGTH: 719
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 39

caatagtcat ggctagaaac cttgaagagg aatcaagtgg tgatacagag ttcattaaag 60

cctcttgtga gacgacgtcg tacccagacc gatgcttcca gtctctgtct tcatatgcaa 120

gcgagatcaa gaagcagcca cgtaagcttg ctgagaccgc gcttgccgtt agcatagccc 180

gagcaaagtc agccaaaacc tatgtatcag agatgactga ttataaagga atcacaaaga 240

ggcagcacga ggctgtagcg gactgtctag aggagatggg agacactgtt gacaggttga 300

gcaattcgct gaaggaactg aagcatctgg aggaaggtga cagcggagaa gacttttggt 360

tctgtctgag caatgtccgg acgtggacaa gcgcagcact gacagatgag accgcgtgta 420

tggatgggtt tggagggaag gccatggctg gggagctgaa aagtttaatc agaacacaca 480

ttgtgagtgt tgcggaagag acgagcaatg ccttggcttt gatcaatgac tttgcttcca 540

agcattgaaa tcatttcaaa ggggtttagt ctttgggaca agagtttttc tcgtattcaa 600

cactgcttgt gttttttttt ctctctttaa agtttctact ttatcttaac ttatcatttt 660

tcatattatg cataaattaa tctgtattaa aattaaaata cttcataatt catttcaaa 719

<210> SEQ ID NO 40
<211> LENGTH: 808
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 40

caaagaagaa gatttccaga gatacgatga gtcgtctgat tcaacattct acgaagctcc 60

aaggtttgtg acacacattg atgatccagc tatagctgca ttgacaaagt attactccaa 120

ggttttgcct cagagcgata ctccaggagt gagcatactc gatatgtgta gcagttgggt 180

cagtcattat ccaccggggt ataggcaaga acgaatagtt ggaatgggta tgaatgaaga 240

agagcttaag cgaaatccgg ttctcaccga gtacatagtc caagacttaa atctcaattc 300

aaatctgcct tttgaagaca attctttcca agttataacc aatgtggtaa gtgtggatta 360

tcttacaaag ccgcttgaag tgttcaagga aatgaacaga atccttaagc ccggaggact 420

cgctctaatg agcttctcga accgttgctt ctttactaaa gcaatctcga tatggacatc 480

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aactggcgac gcagatcatg ctctcattgt tggatcatac tttcactacg ccggaggatt 540

tgaagctcct caggccgttg atatatctcc aaatccaggg cgttcagatc ctatgtacgt 600

tgtttactct agaaaactcc ccatggttta aacctgagat ccaagcacat catgtataca 660

catagtagag accgaggaaa ctaattcttc gattaagaca agggaacttc tgaaatcttg 720

tttataaaga atgtgccact ctctcaacac taataacaat gtcatataaa gaatctgaag 780

ccagattcgc aaatttgacg ataaaaaa 808

<210> SEQ ID NO 41
<211> LENGTH: 626
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 41

ttttttgga agaaagtgta aatacttgaa acttttcaat ctaaaggttt tcacagttga 60

tgtgatctca aataacaaaa aaaggtaata cgaactcata aactgttgtt caaaaaggga 120

accagagaaa cattgtcaat ctaattcagt ttagatgaag aggctgcaaa acccgaactc 180

aatcttgtgt gtcgtttcac catcctcctt tgcagctgaa gttccctcag aatatgtgca 240

tcaagtcata agcaaatgtc cagaacagca caaacgacat aaggccacca agaaagccgt 300

caaaaaggac ccgattccac gaatcaaagt acaagtcagc tgagaatcct gccttagcca 360

tgagcccaac agatgtgatc aacatcacca caaagtaaaa tacaaaacca atcaagccat 420

tgaatccaat tattcctgct aagacaccag ctatgataga cagaaacgtc cggctgtttt 480

gaatgacttt caaattgttc tgcaaattct ctgcactgaa agttggtatg tcactcatga 540

tatcctttga tctcttctca gatgaaccca tttaagatag caacaataat tagaaacgag 600

agtagtaaga ggaagatcga agtagc 626

<210> SEQ ID NO 42
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 42

ttttttttt tttttccaaa aaggttcaaa atcataacac aaaacaaaag aaataaacag 60

gaagctcgag tgccaagtac ctccgccacc tccgatcaag aacccaattc cgagaattga 120

gctccgacgg agaataaacg aagcggtaac acaaacaacc aaccaaatac caaactacta 180

aagtaaagaa actaaaatag tccttcattt catcagcgga aagagttttg atgttcagag 240

ttcacttggc acccttcttg a 261

<210> SEQ ID NO 43
<211> LENGTH: 725
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 43

gatatgagta gccaaatcgc tttgtcaccg gccatcgccg ccgccattcg ccgtccgtcc 60

tctcacgact gtctatccgc ttccgccact actgctaccg ccacccccat ggctctcaaa 120

tcttgcatcg tcgcacctct ctcgctattc acctctcaat ctcaaatcaa acactcaagc 180

tcaagaaaaa cttctcgaac cacgattcga tgcgatgtag cgataaaatc cgcagattcg 240

-continued

ataaacgcag acgccaatcc ttcgtcctca ccgtcatcag aggaagaaat cgaagcggaa 300

gcgaaggcga agataggatc tagggttaga gtaactgcac cgttgaaggt ttatcatgta 360

aatcgagttc cagaggttga tttagaaggt atggaaggta aactcaaaga ttacgttgct 420

gtttggaaag ggaaacgaat ctcagctaat cttccttata agattgagtt cttcaaagaa 480

attgaaggtc gtggtcttgt taaatttgtt tcacatctta aggaagatga gttcgagttc 540

attgatcagt gatgaaacaa gaaagacaat ttttgttttc ctttctcagt gtttgttttt 600

gtttgttgtg tttactggaa cctgggaatg gagaatgatt tgtatgtagt gtgatgtgta 660

ttcaaccttt agcaatcata tacataaggg tttcttcaaa aaaaaaaaaa aaaaaaaaaa 720

aaaaa 725

<210> SEQ ID NO 44
<211> LENGTH: 983
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 44

tctttcttct tcctgattgg aattttaggg cttttgaaag cacgaacgcg tgaagctcta 60

atcgagaaaa aaatggaggt tttggatagg agagacgatg agatcaggga ctcgggaaac 120

atggacagca tcaagtcaca ctatgttacc gactctgttt ccgaggaacg ccgctctcgt 180

gagctcaagg atggtctcca tcctttacgg tacaagtttt cgatatggta cactcgtcgc 240

acaccagggg ttcggaacca gtcttatgaa gataacatca agaagatggt agaattcagc 300

acggttgaag gattttgggc ctgctactgt caccttgctc gttcttctct cttgcctagt 360

ccaacagatc ttcatttctt taaggatggg attcgtccat tgtgggagga tggtgccaac 420

tgcaatggag gaaagtggat catacgtttc tcaaaagttg tatctgctcg cttctgggag 480

gatctgcttc ttgcgttggt aggcgaccag cttgatgatg ctgataacat atgtggggca 540

gtactgagtg tccgtttcaa cgaggacatc attagtgtat ggaatcgcaa tgcttctgac 600

catcaggcag tgatgggttt gagagactca atcaagcggc atttgaagtt gcctcatgca 660

tatgtcatgg aatacaagcc acacgatgct tctctccgcg acaactcttc ctacagaaac 720

acatggctga gaggataggc ccaaagtcga tgattgtatc atgtaatgtg gagaagattt 780

gggaagctca tctgcaacct gggaagatat ctggattgaa ccctgtatcc aataccatac 840

tgtaccggag gcttacaata tcagaaaaac aaaatccggg ctacttctgt gtcagtatgt 900

gttcatttcg tttttctttt acagtacatc ttgttaactt caatggtttg actcttgatc 960

aaaactataa gggttaattt tca 983

<210> SEQ ID NO 45
<211> LENGTH: 693
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 45

aaagacgctg aagaagaact ttgccaacaa gggtcttaac gctaaagacc ttgtggttct 60

ctcagggggt cacaccattg gaatctctag ttgcgctctc gtcaacagtc gtctctacaa 120

cttcacagga aagggcgatt ctgacccatc catgaaccct agctacgtga gggaattgaa 180

gagaaagtgc ccgcctacag atttcagaac ctcactgaac atggacccag gcagtgcgtt 240

-continued

gacattcgac actcactact tcaaggtcgt ggctcagaag aaagggctct tcacatctga 300

ctctacgctt ctcgatgaca ttgagaccaa aaactacgtt cagactcagg ccattctccc 360

tcctgtgttt tcttctttca ataaagattt ctccgattcc atggtcaaac ttggtttcgt 420

ccaaattctt accggcaaaa atggtgagat caggaagaga tgcgccttcc ctaactaatt 480

tggatcgatc agaccgggtt tcggatgatt ttgagtctac acgtttttct ctgcttattt 540

tctttctttt tctttttttct ttcacggaag tttgagcttt ggtgttgtct tcttctgttt 600

cttccatgaa taattgtttt ttgttgagta actttacatt tgtattcttt acggtgactg 660

tgttttgtaa tggaaaaagt ttgtttcgaa ttc 693

<210> SEQ ID NO 46
<211> LENGTH: 903
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 46

ttaaaccaaa gcatactctt ttgccagaga atcatcaaga catgacgatt atttcaatgg 60

tgactctatc agggaaccaa gaaactatga taacaatttg gaagctccta caagaaacac 120

tctggtacaa tccctccaat ggagagagaa aacacctact caggacaatc caatctttga 180

aacctcccag tcctccagag tcaggcgccc acctcttgag agacagcagt cgacactcta 240

accctcacaa cttcgcctct catcccaact acagaagccg taatgggaga actctgtgat 300

gtcactattc aatacacgag ctgcgccgat cctagcaatt ccctctcctt ttgataacca 360

tttctctgta gaacagcctc tctctcctga tgtgccagta catcctgctc agatacaaca 420

gatccctccg atcccaccaa agaaaaagaa gggccgacct ccacttacaa aacctattag 480

acgccatggt gatgactctg tcagcacttc aagtaaatcc tcttctcaga gacgacaaca 540

caccagggtt gcagcaaatc tggcttcttc aagcaaagct cctcctacaa ggccaattat 600

cccagccact gtgaaaggaa gggtggattt tcccaatcca cctcctcctc ttccttaaaa 660

cttgcaagct ggaactgctg tgggctgggg aatcccatga cagttcaacg actgagagag 720

attcagaaaa caatctctcc agacatccta ttcctcatgg agacgaaaaa ccctgatgaa 780

gtggtgctta aaaaacttca atggtcgaat ttctcaaacc atttactcat atctccgcac 840

agccctgggg gtggaggcct ggccctctac tggaaacaac acatcgagct agaagtactc 900

tcc 903

<210> SEQ ID NO 47
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 47

gtaaccatgc cttctctcta cgaaaaatcg gaacttttct ctgtcacaga gaattttcta 60

aatccgagat tcacctggac cattcgggga ttctctacgc tgctaaaaaa cagttaccta 120

tcagaagtgt tctccatcgg aggaagaagt tggaatatac aaatcaatcc aagtggtctt 180

ggtacgggag agggaaaagc tttgtcgatg tatcttggcc ttaatgtgaa tgagatattc 240

agaccatatg agaagattta tgttcgagcc aagcttcgag ctcttaacca actcaatctc 300

agtaacatcg aaagggaact cgatatttgg tacaatggtc cgggatatgg agaatatagc 360

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tggggtttcc ctgagtttat ctatttccct tatctcacag attcatcaaa gggtttcgtt 420

aagaacgatg tgttgatggt tcaagttgaa atggaggcca tttcttcaac caagtacttc 480

ccgagttaga ttttctctaa gcaaagaact tgtacctacc tccatgtgtt tgatttgtta 540

tcaaatacta ataagaattt gattatgcat ttcaaataca attgtttctt tttcttaaaa 600

aaa 603

<210> SEQ ID NO 48
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 48

ttttttttgt tataagaaag accgattgat ttatatgtaa caccaaaaca acatagagaa 60

aaccaaaagg aacaagcaag agcttcccac ggcagacatt ctagaaggat gatttactca 120

aagatatcat catcgtcatc ggggaggggt tgag 154

<210> SEQ ID NO 49
<211> LENGTH: 162
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 49

gaagaagcag ctgaagctgc taaatctgct tgaaaaaacc cgctattgat ttatggtctc 60

ttccttgttg tttcctcgag atgttgttaa tctctgttat ttgttgctga accatcttgt 120

atttgttttt cttttggtgt aaacactttc cttatcaagt aa 162

<210> SEQ ID NO 50
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 50

ttttttaaaa tttaaaaaca tattttcaaa tcaatgtaaa atagaaacgt tgaagagaga 60

aacaactgaa gaatgggggc aaagcgccag aaacttgtaa aaacaagtaa aaggattggc 120

aaaagtaaga aagcacacca ctttaaaact aacattaagc tttggatgat gatgattctt 180

cttcgtcatc ttcatcaatg tcccaactta aatcttcatc ttcct 225

<210> SEQ ID NO 51
<211> LENGTH: 1261
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 51

tgaaaccgga aatgtagtaa cttgacataa gtttttcaat ccgacaataa aagtgatccg 60

agttcgaatc tatcaaaaac caaacgacaa aaactaatca cgacgacata gcgttgttga 120

ctacaaacag ttacaacatc ctactttgat agagattgtg gatccactct tatcactcgt 180

cagctggtgg cgaacgagga gaccggctct tctgcattgg gctctctgca ccatcatacc 240

caccatcact gtctcttctt cctattgacc cagggctttc aacttggcca ttctcggggc 300

tagacctcga tctctctctc ctttcaatgg gactttcaac ttcaccaacc ccatttctcg 360

gactctcctt cttgaacggg ctgtgattag ggctcatcct ctctctcttg ttgttgggac 420

-continued

tgcggctgta cttagtaggg cttgcgactc tctccctcct gcgagggcta tcattgcctc 480

tgcggtcacg accatactcg ggactgccac gtcttgattt cttgtaagga cttgggctac 540

gtcttcgacc atagtcagga ctggtccttt cctttctgta ggcagcaaca ggactagctc 600

ctcggccata atcagggctt cctctttctc ttttgtaagg actaggtgat cgccttctcc 660

tttcaggtga cctatcacgg cgtctttcag gactgtgtcc atttcctcta gcatcatcat 720

ccttcacagc atactccacc gagatcacct tatccatcag cttactgtta tttgaagcat 780

ccaatgctct ggtggcatcc tcttgtgcct cgtactggat aaatgcaaaa ttcctcctga 840

tcctaacgtt tacgatcttt ccatacggct caaagtgttt ctctagatcc cgggtcctag 900

tattatccgc atcaaagtta atcacaaaga gagtcttgga aggtctcatg ctggatgagg 960

atctccttga accaccacca gatcttttat cacctccacg ttcactcttt gtccattcaa 1020

cacgaagtct gcgtccctta cgcccaaatt caaagcggtc aagtgctcgg atggcatctt 1080

ccgcatccct ttcatcttcc atgtatacaa aagcaaaccc agctttcata tcaaccctct 1140

caaccttgcc gtatttcctg aatagtcgtt ccaggtcacc ttcgcgcgca tcatactcaa 1200

agttcccaca gaagactggc ttcatgcttc ctgtagaatg attttggcag gcgtagtcgc 1260

g 1261

<210> SEQ ID NO 52
<211> LENGTH: 745
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 52

acgataactc cgccgtctcc cgccgtcttg ctctcactct cctcgtcggc gcctgctgtt 60

ggttccaaag tatctcctgc tgatgccgcc tacggtgaag ctgcaaacgt gtttgggaag 120

ccaaagacga acacagactt cttgccatac aatggagatg ggttcaaagt gcaggttcca 180

gcaaaatgga acccaagcaa agagattgag tatccaggac aagtccttag gttcgaagac 240

aacttcgatg ctactagcaa tctcaatgtc atggtcactc ctaccgacaa gaagtccatc 300

actgattacg gttctcccga agagttcctc tctcaggtta attacctcct agggaaacaa 360

gcttacttcg gtgagactgc ctctgaggga ggctttgaca acaatgcagt ggcaacagca 420

aacattctgg agtcatcatc tcaggaagtt ggtgggaaac cctactatta cttgtctgtg 480

ttgacaagaa cggctgatgg agacgaaggt gggaagcatc agctgatcac agcaaccgtg 540

aatggaggga agctttacat ctgcaaagca caagctggag acaagaggtg gttcaaggga 600

gccaggaaat ttgtcgagag cgcagccact tctttcagtg ttgcttgagt gaaagcaaca 660

caacgtaaca atgctctgct tgctttcttc atttgtctct tgtaaaaaat ggaaaatgaa 720

actgagcttt tgagaaaaaa aaaaa 745

<210> SEQ ID NO 53
<211> LENGTH: 725
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 53

gatatgagta gccaaatcgc tttgtcaccg gccatcgccg ccgccattcg ccgtccgtcc 60

tctcacgact gtctatccgc ttccgccact actgctaccg ccacccccat ggctctcaaa 120

-continued

tcttgcatcg tcgcacctct ctcgctattc acctctcaat ctcaaatcaa acactcaagc 180

tcaagaaaaa cttctcgaac cacgattcga tgcgatgtag cgataaaatc cgcagattcg 240

ataaacgcag acgccaatcc ttcgtcctca ccgtcatcag aggaagaaat cgaagcggaa 300

gcgaaggcga agataggatc tagggttaga gtaactgcac cgttgaaggt ttatcatgta 360

aatcgagttc cagaggttga tttagaaggt atggaaggta aactcaaaga ttacgttgct 420

gtttggaaag ggaaacgaat ctcagctaat cttccttata agattgagtt cttcaaagaa 480

attgaaggtc gtggtcttgt taaatttgtt tcacatctta aggaagatga gttcgagttc 540

attgatcagt gatgaaacaa gaaagacaat ttttgttttc ctttctcagt gtttgttttt 600

gtttgttgtg tttactggaa cctgggaatg gagaatgatt tgtatgtagt gtgatgtgta 660

ttcaaccttt agcaatcata tacataaggg tttcttcaaa aaaaaaaaaa aaaaaaaaaa 720

aaaaa 725

<210> SEQ ID NO 54
<211> LENGTH: 725
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 54

gatatgagta gccaaatcgc tttgtcaccg gccatcgccg ccgccattcg ccgtccgtcc 60

tctcacgact gtctatccgc ttccgccact actgctaccg ccacccccat ggctctcaaa 120

tcttgcatcg tcgcacctct ctcgctattc acctctcaat ctcaaatcaa acactcaagc 180

tcaagaaaaa cttctcgaac cacgattcga tgcgatgtag cgataaaatc cgcagattcg 240

ataaacgcag acgccaatcc ttcgtcctca ccgtcatcag aggaagaaat cgaagcggaa 300

gcgaaggcga agataggatc tagggttaga gtaactgcac cgttgaaggt ttatcatgta 360

aatcgagttc cagaggttga tttagaaggt atggaaggta aactcaaaga ttacgttgct 420

gtttggaaag ggaaacgaat ctcagctaat cttccttata agattgagtt cttcaaagaa 480

attgaaggtc gtggtcttgt taaatttgtt tcacatctta aggaagatga gttcgagttc 540

attgatcagt gatgaaacaa gaaagacaat ttttgttttc ctttctcagt gtttgttttt 600

gtttgttgtg tttactggaa cctgggaatg gagaatgatt tgtatgtagt gtgatgtgta 660

ttcaaccttt agcaatcata tacataaggg tttcttcaaa aaaaaaaaaa aaaaaaaaaa 720

aaaaa 725

<210> SEQ ID NO 55
<211> LENGTH: 724
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 55

agtaaacgag caaaagaaga agagaaacaa caagaagtag taatggcttc ctctatgctc 60

tcctccgccg ctgtggttac atccccggct caggccacca tggtcgctcc attcaccggc 120

ttgaagtcat ccgctgcatt cccggtcacc cgcaagacca acaaggacat cacttccatc 180

gcaagcaacg ggggaagagt tagctgcatg aaggtgtggc caccaattgg aaagaagaag 240

tttgagactc tatcttacct ccctgacctt agtgacgtcg aattggctaa ggaagttgac 300

taccttctcc gcaacaagtg gattccttgt gttgaattcg agttagagca cggatttgtg 360

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taccgtgagc acggaaacac tcccggatac tacgatggac ggtactggac aatgtggaag 420

cttccattgt tcggatgcac cgactccgct caagtgttga aggaagttga agaatgcaag 480

aaggagtacc cgggcgcctt cattaggatc atcggattcg acaacacccg tcaagtccaa 540

tgcatcagtt tcattgccta caagccccca agcttcaccg aagcttaatt tcttttctaa 600

aacattctta tgaattatct ctgctcattt catttcctat tgtctgtgtt ctttttctct 660

ttatgagaca atttctatcg gattgtcaaa tgtctgattt atgaatatgt aatttatata 720

aaaa 724

<210> SEQ ID NO 56
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 56

agccaggaga atactctcct atgccacatc attcgtcttt atcgaccagt atgggaccat 60

catcgtacga aggcagagag cggaagagca gtagtatgat tcaacacgga ggttatcttg 120

aagagccaag catcagactt cttggaaaag aagcttccag caaaatggct cgtcgtgatc 180

ctgacccaat ctatgaccgt gaatgggaag acgacaagag gagagcagaa aggaagcgga 240

gagatcggaa gtagagagtg atgatttgca gatcctttgg tttgttcaac gaagagagag 300

acaaatactg gtattgaaca ctgcttatgt tgtacacgta ctattcaatg accgtgcggg 360

tctactttgt catttggctc cgccgagttt gataaatgac ttgccagact tcagat 416

<210> SEQ ID NO 57
<211> LENGTH: 145
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 57

aatctttgtt gttgtaagat gttataagga tctcaagcac ctattattct taaatattat 60

tggttgatgt tgctagcaag aaaaattgaa tacaacctta aaaaaaaaaa aaaaaaaaaa 120

aaaaaaaaaa aaaaaaaaaa aaaaa 145

<210> SEQ ID NO 58
<211> LENGTH: 299
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 58

gagatggctg catcgcataa ccggaagctt gttcaacctc ccgaaggaac tttcttctaa 60

tactctcaaa gcctaccttt gaggggcttc tccattgttg gtcttcaagc ttttctttcg 120

taccttaaag taaaaacaat ggtgtctgtc gatgaatgat gatgttcgat tgatcatctg 180

gagtttaaat ccttgtgtgc aaatatatct agacaacgct gtctcacgac ttcatcttct 240

cagtttagat ataatatggg aaacaacctt ctagaaaaaa aaaaaaaaaa aaaaaaaaa 299

<210> SEQ ID NO 59
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 59

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ttttagaga gtcaaattag aatcttgttt caaataccat cttcaaatgc aagagatagt 60

aagagagctc aaaaggttaa accaagaaag taaaatgaca ttattaaggt cgacgagaat 120

gtacaatcat caagaggatc agacgtagaa gctgaggtaa ttagcagtag aaagatccac 180

caaatgtgtt ctctccactg tatgtcatgt agagaaaccc gtcttcgtct ttgtgttctt 240

cgtagattgc agacatcaat gccgcagttg gtggtaatgt gttcttgaca aagacaaaga 300

tggctttttc agctccaagc ttgattcttt tcctcacaac gtacacaaat tggccaatgg 360

ttagatcagc tggtacaaga tacttcttct tgtcaatgtc aggaacatca ctctgtccag 420

cttttccaca atcacgggaa ctctttcagg 450

<210> SEQ ID NO 60
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 60

ctatagagaa tcttcaagca ttagaaggat ttgtgaatca agcagatcat ctgaggcaac 60

aaactttgca acaaatggcg aagatcttaa cgacaagaca atcggctcga ggtttactag 120

ctttaggaga gtatcttcat agacttcgtg ctcttagttc tctttgggca gctcgtccac 180

aagaaccaac ttaaaagagg aacttattaa aactttaaaa acaagaaaca gcagaatcaa 240

aagtcttgaa gaagcatact catcacaaag cttggaagga tgttttaaaa aagatctttg 300

ttaattaagt agagtgagat tctcttgatt agaactttat ggtttttgct ttatgaagta 360

tctctccaga gaagattgta aatttgggtt gaaactttgt aatatattta gatacaacaa 420

ataagtttg 429

<210> SEQ ID NO 61
<211> LENGTH: 1012
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 61

ttttttgcg taatgtagtt tcctacgttg ttgtatctat aaatagtttg tttctcgagc 60

ttccatttca taattcctca tttcccggat ctctcccatc taaaaataac ccgacccatt 120

tacgcgaccc aaaccggatc aacccgcaat ggataagcca agcttcgtaa tccaatccaa 180

agaagcagaa tccgccgcga aacaactcgg cgtttccgtc attcagctcc tcccgtcgct 240

agtcaaacca gcacaatcct acgctcgaac tccgatttcg aaattcaacg tcgcagtcgt 300

cggactcgga tcatcaggtc ggatcttctt aggcgtcaat gtcgaattcc caaatctccc 360

tctccaccac tcaatccacg ccgaacagtt cctcgtcacc aatctcacac tcaacggtga 420

acgtcacctc aatttcttcg ccgtctccgc cgcaccatgt ggccattgcc gtcaattcct 480

ccaagaaatt cgcgacgcac ctgaaatcaa aatccttatc accgatccaa acaactccgc 540

cgattccgat tccgccgccg attcagacgg attcttacgt ctcggaagct tcttgccaca 600

cagattcggt cccgacgatc ttctcgggaa agatcatcct cttcttctcg aatctcacga 660

taaccatctc aaaatctcag atctggattc gatttgtaac ggaaacaccg attcatccgc 720

cgatttgaaa caaacggctt tagcggcggc gaatagatcg tacgcgccgt atagtttatg 780

tccatcggga gtttcgctgg tggattgtga cgggaaagtg tacagaggtt ggtatatgga 840

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atcggcggcg tataatccta gtatgggacc agtacaggcg gcgttggttg attatgtggc 900

taatggtggt ggaggaggat acgagaggat cgtcggagcg gttctggtgg agaaagaaga 960

tgcggtggtg aggcaagagc acacggcgag gttgttatta gagactatat cg 1012

<210> SEQ ID NO 62
<211> LENGTH: 605
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 62

caaacatcag aagccctaga gcttgagccg tcgaaaatgt cgaagcgagg acgtggagga 60

acgtctggta acaaattcag gatgtcactt ggtctgcccg ttgcagccac agtgaactgt 120

gcagacaaca ctggtgctaa gaacctttac atcatctctg ttaaaggaat caaaggtcgt 180

ctcaatcggt taccttctgc ttgtgttggt gacatggtta tggccactgt caagaaaggt 240

aaaccagacc tcaggaaaaa ggttcttcct gctgtgattg ttaggcaacg taagccatgg 300

cgccgaaagg acggtgtttt catgtacttt gaagataatg ctggagtgat tgtgaaccct 360

aagggagaaa tgaaaggttc tgcaattact ggacctattg ggaaagagtg tgcggatctc 420

tggccaagga ttgctagtgc tgctaacgcc attgtctgaa gatcatttat cacttttgct 480

ggttatgtat ctgtcttcaa cgaaacgcga aatagttggt gttttgagtg ttttaagtag 540

agacgacaat cttttgtgag cttcagacat atttccagtt tctaagagat tttgcttaga 600

ttaaa 605

<210> SEQ ID NO 63
<211> LENGTH: 915
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 63

ttttttttt tttccaacca caacgagatg aattacacca cgactctaag tgaaatcatc 60

ttttaaacca ccaaaattca cccaatgaca cgaaaacatt tctagcacaa agaaaatcaa 120

atcctatcct gagatccaat ccaattccaa gctattagtc cctcatgatc cgagtgtaga 180

acatgtccta atagcatcta cgccaaaagc gcaacttcag aagggttttg actcctctgc 240

tttcactatt tcggtcctaa gcctaaaacg gacatactaa tccgactgat actcaaccgg 300

atcaaccggg ctgagacaaa aatttcttga agtcgaggct ttattggaga gctttccttc 360

ttcttctaca atccaaatgg ttttcttttc tcccccattt ctcattaatt ctccatcagg 420

agtcgttgac ggcagcatag ctaatacgcc ttgaatcatg taaatctgcc cgggatcgat 480

aggatcttca caaccaagct cgaaaaccac gatccgccta cctctgtacc ttcttaacac 540

tgagccacca ctaccaagga ggttcatcgg aggagaggta cctccgcgaa gagactgacg 600

aagaaatcca ccagatctgc tgccgtcgtc gagagtcata gttccccatt gtagatctac 660

caacgaacct ccatctgaga gaactatctc cgctcgccgt cgacttaaaa ctctttgatt 720

aagccacaaa gaaggaggag ccgccgccgg ctaaaaaaaa tcgacacaaa ggaaaaaaaa 780

aactaaaaag agaagagagg ccctctcacg gtgccggccg aaaccgacca ccaaagaggc 840

aaaacggcgt ttgaagattt gatctggttt gcggcggcta actagagaga gagaactagg 900

gttttttgtt tagtt 915

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<210> SEQ ID NO 64
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 64

ctatagagaa tcttcaagca ttagaaggat ttgtgaatca agcagatcat ctgaggcaac 60

aaactttgca acaaatggcg aagatcttaa cgacaagaca atcggctcga ggtttactag 120

ctttaggaga gtatcttcat agacttcgtg ctcttagttc tctttgggca gctcgtccac 180

aagaaccaac ttaaaagagg aacttattaa aactttaaaa acaagaaaca gcagaatcaa 240

aagtcttgaa gaagcatact catcacaaag cttggaagga tgttttaaaa aagatctttg 300

ttaattaagt agagtgagat tctcttgatt agaactttat ggtttttgct ttatgaagta 360

tctctccaga gaagattgta aatttgggtt gaaactttgt aatatattta gatacaacaa 420

ataagtttg 429

<210> SEQ ID NO 65
<211> LENGTH: 574
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 65

ttttttttttt ttttttttttt ttttttgagg agaaataatt ggtaaacttt tgcggtacat 60

acggtttggg tcaagttaca aacggataaa ccggtataga atacacagag tttttgaatt 120

ctcccattta agctgcaact tcttcgacct catccaatgc atagttgttg gtcgatatgt 180

tggcgtaatt gacttttgcg aaccggacca caaccgggta tcgagtctta gggtcctgat 240

caacggcaac aactgatcca acgttcttga accaatagga ttctctcctt agaatcttga 300

ccttagaccc tctcttagga ccaatcggtg gtggcttggg tttggtggca gtagctccat 360

ccggagcagc ggcagctgcc ggagaatctt ttgaagaaga ggaagccgga gcaggatctt 420

cggctgccct gactacgagc ctagaaccgg cgtttctcat cggcaagaaa gacacggagc 480

tcctggacga cgaagcgccg gcgaccgagg tgacattggc cggtagaaca aataccgtag 540

atgctgtcgt catcgccatc tctggttttc tttt 574

<210> SEQ ID NO 66
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 66

ttgtttttttt tttgtttttt ttttttttttt ttttttaaga aaggcgattt gctcaccata 60

atcacaacat attcaagaac caaagacaac gaggtgacat aaaaaaacac caaaaaaggg 120

actcaaaaca tgaagaaaca aaagagaaga aacaagaaac ttgaagaaac aaggccatta 180

actccgaatg cataagctcc tgagttagta gttgttaaaa gagaatagcc gccttccggt 240

gtgtttgtag tgaggatgac aacaacccaa atatcaccag aaccaatacc aattccagtg 300

atcttagaat cattcaagtt cttgagtacg acactgttga aattgctcaa gtcagggttc 360

ttatcatgct taggaaaaca gacttgcatg atcacaccgt ctctgactac ggttgtgttg 420

agactgcatt tagcgaggag gttatttcca gggactggag ctgagttatt agtgtttgtg 480

-continued

cagggttggt tctttagttg gtctacgact tcgtctgcga gacattctgc gttttcgttc 540

tttgttaagg tttttaggtt tagtcctgtt ctgtatttgt tgaatactgt aagaagaagg 600

tcttcttctc catcggtgcc ggaaagaaca agacgatgaa gggagagaaa gactgagaga 660

agacagagta gatggagttt ggaaatcgcc attgatgcag aggtttttt tttt 714

<210> SEQ ID NO 67
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 67

agttacatcg agtaacgcag caacatttgg ggtcggggct attcaggtag tagcgactgc 60

aatatccact tggttggtgg acaaagcagg tcgtcggctt ctgcttacta tctcttcggt 120

tgggatgacg attagccttg taattgttgc agctgctttc tatcttaagg aatttgtgtc 180

tcctgattca gacatgtaca gttggctgag catattgtca gtagttggag ttgtggcaat 240

ggttgtcttt ttctcattgg gaatgggacc aataccgtgg ctcattatgt ctgagatcct 300

tcctgtgaac ataaagggtt tagctggaag tattgcaact ctagccaatt ggttcttttc 360

ttggttgatc accatgacag caaatttgct gttagcctgg agcagtggag gaactttcac 420

tctgtatgga ttggtttgtg cattcacagt ggtgttcgtg actctatggg ttcctgagac 480

caaaggcaaa actcttgaag aacttcaatc cttgttcaga tgaacaaatt gaaacaactt 540

cattctttgt caccctctct ctccctctct gttttggcca agaacaagaa gaaacaagag 600

attttccagc tttgttaatt gggctgagaa cgttactaag atttgtttgt ttgttcgttg 660

tgtgtcaata atcgcattat cttctatcac atgtatatca acatactaca ttcaagtatt 720

tgtaatttta ttgaactctt tacatagagc aaaggttttg ccaaaaaaaa aaaaaaaaaa 780

<210> SEQ ID NO 68
<211> LENGTH: 641
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 68

gaacattcag aacaagaact catcctactt tgtggaatgg atcccaaaca acgtcaagtc 60

cagtgtctgt gatattgcac caaagggttt gaaaatggcg tctactttca ttggtaactc 120

aacctcaatc caggagatgt ttaggcgtgt gagcgaacag ttcacagcta tgttcaggag 180

aaaggctttc cttcattggt acacaggaga aggcatggac gagatggagt tcactgaagc 240

agagagtaac atgaatgatc ttgtcgcaga gtaccagcag taccaagatg ctacagccgg 300

agaggaagag tacgaggagg aagaagagga gtacgagact taagatgttg tcaatggctc 360

cctcggattc gtaagctgtg taagcaagca gcattcactt tcttctttcc ccttatcctg 420

aatttttttc ttcgtaatat ctcttttatt gtttcgttca tgtgtgttcg tttttgttat 480

tgaaacccta tatcggttct ggatttgtta aacttttgcg tgtattgctt attgtttttg 540

tcggtgaaaa aaatattgct tttgttctct taagttttgt gttgccaaaa aaaaaaaaaa 600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 641

<210> SEQ ID NO 69
<211> LENGTH: 503

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<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 69

ttttttttca gcccaaagaa cacttttaa ttactagtaa agtttaacta acggttaata 60

aacttacatc agacaatatt acacttttta tcttggctgc ttcaatgtct ccgcatcgtt 120

cgttttaccg gtgaaagaag cttcttagct ttcctctttc aagcttctcg agaagcttat 180

cggcgcccat tacttccatc tccgacagct tcttcagata ccctattgct ccgtacgaca 240

ccatcatttt cttactcttc tcgcttcccg acatccccaa cagccccgcc acggcgtact 300

tcttcgccgt gtttccaggg tttgaatcca ataacatcac caaattcgtc agaacgctct 360

tcccgtcttt cttcagttcc cgtcgaatcc ttccttccgc taccaatcca gcgatcgcct 420

gagccgccgc ttctcgacat ccgtttgact tcgattccag aagtttcacg atctccggga 480

tgcaaccgga ttctcccact agc 503

<210> SEQ ID NO 70
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 70

ttttttttca gcccaaagaa cacttttaa ttactagtaa agtttaacta acggttaata 60

aacttacatc agacaatatt acacttttta tcttggctgc ttcaatgtct ccgcatcgtt 120

cgttttaccg gtgaaagaag cttcttagct ttcctctttc aagcttctcg agaagcttat 180

cggcgcccat tacttccatc tccgacagct tcttcagata ccctattgct ccgtacgaca 240

ccatcatttt cttactcttc tcgcttcccg acatccccaa cagccccgcc acggcgtact 300

tcttcgccgt gtttccaggg tttgaatcca ataacatcac caaattcgtc agaacgctct 360

tcccgtcttt cttcagttcc cgtcgaatcc ttccttccgc taccaatcca gcgatcgcct 420

gagccgccgc ttctcgacat ccgtttgact tcgattccag aagtttcacg atctccggga 480

tgcaaccgga ttctcccact agc 503

<210> SEQ ID NO 71
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 71

gattcgataa gaagaatcta catggctcga catatcatgg agaagttcat cgtcgcagga 60

gcggaaatgg aattgaactt atctcataaa acccgacaag agatcttaac cactcaagat 120

ctaactcaca ctgatctctt caagaacgca ttaaacgaag tcatgcaatt gatcaagatg 180

aacttggtaa gagattactg gtcatccatc tacttcatca agttcaaaga agaagaaagc 240

tgccacgagg caatgcataa ggaaggatac agtttttcat ctccaagact gagttcagtt 300

caaggctctg atgatccttt ctatcaagaa catatgtcaa agagttccag atgcagtagt 360

cccggttaag gagtctaaaa ctggtactag accagaaccc aaaccaatgt tcatagcaat 420

ccaatccatg taatcttcct tcacatttct tgtacatgtc attttctctc ttgttatacc 480

taactgtaag agaaaatgtc cggttcggat tttggtttag ttttaaatgt gtataccgga 540

caaaaactat ggaaccatac taattaatat ctcgaaga 578

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<210> SEQ ID NO 72
<211> LENGTH: 679
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 72

tgggtttttg ttttgaactc tccttatgta ttaccgcctc gccggagact gatacagttt 60

cttctgtccc tcattgaaag aagaaaagaa aacaaaaata gaaaaaaaaa gaaagcagaa 120

aaaaagccta ggaggaacaa tgaatttaga aaaccaaacc atgacagaaa agtctgcggg 180

attctctggt tagctctagg tgatgatatg atcaagtttc gtcctcactg gctttgtatg 240

aagggaaaag aagataatct aaaagattcg ccaaaagaca cagatcgttc accgtgatgg 300

ctcgcctaca atatcgtggt aaaacaaaaa cgattgtact aagtagcaat tcctctgttt 360

ggttgtctct tgttcacact gtaactgcca acataacctg gagatgaact tctagctgaa 420

acatctgaag aaggaacccc tcctccaatc ccatagctaa aaggagcagg cccttctgtc 480

tcaggagttg gtgatctcca tgtagggtca ctataaactg caccattccc gtaaaactct 540

gcaagtcctg ctgtatcata acccgtgttg ttggttgctg aggcagaaga gaatgaagag 600

gatggtgctg ccttgttagc ccctgggttt cttgctgcat aaccacctgt tcccaaccca 660

aaaccagatt caccgtttc 679

<210> SEQ ID NO 73
<211> LENGTH: 599
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 73

ctcggtgagg ctgtcggtgt tgaagggctg gttgtcggtc tgcgcgctca gcgccagcag 60

cgcgcgccgc gagaagcagg taccgacacc ggccgacggc accatgccgg aaacactttc 120

gcgcaccacc agatccttgg catgccattc ggcgaactcg tccatgtaga cgccggccac 180

cagttcgtac cactcgcggt ccagcgaggt gaccggcaac tggatcatgt ccttgcgcgg 240

caaaaggtag ttgtagaagc gcagttccat cgggtgcagc acgtcctcgc tgtcgtgcag 300

gatcaccccg gcgaactcga tgtcgtggcg cttctcgtaa tcgaagatgg ccaggatcag 360

ccagttcagg cagtcggcct tgctggtcgg cccgtcatgc ggcacttcca cgcggcgcag 420

gcgcttgtag cggcggcgca tgcgctccac ttcgtcgatg gtctgctggt cgttgggata 480

ggtgccgacg aacacgacgt actcgcggta atcgagtacg ttgatcatgt tctccaccat 540

ctgcgcgatg acgtcgtact ccatccacgc cggcaccatg atcgccagcg gctgttgcg 599

<210> SEQ ID NO 74
<211> LENGTH: 997
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 74

ttgatttaaa aacagttggt ggaaagctta ctttgtacca aacgacccta tgcgagagaa 60

tctcagggga taacattgat ctcgggctag atctcgggtc tcaaagcttt ttgccaacat 120

acaacaaaaa tgacatccag ctgatatgct gtcaagctga tgcaagtgtt ttatggcttg 180

tccctgacac agttgtgacc agatttattc aatcccttga ctgggacaca gatatggaca 240

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tcacctttac ttgggttctt aacagagacc gccctaaagg caaggagact gtgaaatatg 300

aaagaagtgt cgaccctctg gaccttccaa aacgctctga tatccaaatg gttctcaatg 360

ggtcgatgga tggatttaga gtgcataatt tgtacccaaa gttcttccgt gttactggtt 420

ctggtgatgt caggtctttc gaggatcaga cggatgaagt gagtgcagac atactcatta 480

accatgcaaa tttcaagtgg tggtggtcat tccataatct taaagcgtct gaaaatatca 540

gcgcttgcga ggggatggat ggaccagttg ctatcataat gtctgaggaa acaccgccac 600

agggctttct gggtgacacc ctcagcaagt tcagtatatg gggactctat atcacatttg 660

tactagcggt ggggcgtttc atcaggcttc aatgctctga cctgcgtatg agaatacctt 720

acgagaacct gccttcgtgt gacagattaa tagccatatg cgaggacttg tacgcggcta 780

gagcagaggg tgagcttgga gtagaagaag ttctatactg gacgcttgtg aagatctata 840

gatccccgca catgctgctc gagtatacaa agctagacta tgatgcttag gtccaaaacc 900

agtctctcac actaaagaaa cactttgtca tatttgtaca tactgagcgg aatattctga 960

gggatttgtt ttgttttcaa tcagcttgta gttgatt 997

<210> SEQ ID NO 75
<211> LENGTH: 329
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 75

acgatgttga tcacaagggg caagagatgg taacaacagt ttgcatgaaa tgccacatgc 60

tggttatgtt gtgtacatca actcctgttt gtcccaactg caagttcatg cacccacacg 120

atcacagctc tacaaaactg tttaaaccat caaatttgct taggcttcta tgctaggctc 180

tttcaaggtt actgaatcta taaaatttgt acggcagata ataagccaag agactagata 240

tggacaaagt tatgtatata ctaaaagtac cagaaagttt gtattaattc tctgcttcta 300

tgaacgatca tgctttagat ctctaaaaa 329

<210> SEQ ID NO 76
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 76

cgctcgcgat ctagaactag gcttttacga acagagagcg agccagagag agtgagtaag 60

agagaatgac gagcgtgagt gggtgtggtt cagtgagtct gataactaac cgcagtgcgt 120

tcttgggaaa cggacttcaa caccgtgccg ttttccttaa accatggtcg tcttcttcgc 180

ttcagtctcg gtccatggtt gtcgaagcca aaaccaaaac cagcagcgaa gacagaatcg 240

cccgccactc tcgtatccgt aagaaggtta atggtacaac ggagaggcca aggctatgtg 300

ttttccgatc aaacaagcat ctttatgttc aagtgattga tgataccaag atgcacacct 360

tagcttcagc ttccactaag cagaaaccaa tctctgaaga gttcgactac acctctggac 420

caaccattga ggtagcgaag aaagttgggg aagtgatagc aaaatcttgc ttggagaaag 480

gtatcacaaa ggtagccttt gaccgtggtg gttaccctta ccatggacgt attgaggctc 540

ttgctg 546

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<210> SEQ ID NO 77
<211> LENGTH: 678
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 77

ttttattaa tagttatttt attaaatttt gaagtactat ttttgtcaat acaaaaattc 60

tgcaacacat tctgcttcag gaagaatgaa atcagtctcc caacaaacaa gttctttacg 120

aataccaagg ggagtgtcgg actgatgtta gccaagttga ttttttttt catcaagaaa 180

ctaaatgctt tctctgagtt tgacaggaag gtcaagatca ggttccgtgg gagtcaaggc 240

acagaagtaa tcatcaacca tgtcctctga tactttctcc aagctcggtg gatcccactt 300

tggtgcttca tccttgtcta tcaatcgagc tcgtactccc tcacaaaaat tgccggacat 360

tggcccgatt aatccttgta gcgacattct gtactctcgg attaagcatt ggtcaagtgt 420

ttgtaatctt ccttcccgga tctgttggat tcgttttaaa gaagagatct caatgccacc 480

ttcaaagata acggtgagct ttctttaagt ctacgtagag tcgtaatgca ccatgtatct 540

tttcttctac tagcctcgat ttccaaagaa tcaataattt cttctactgt gtcatggcta 600

aagcattttt caagtaaatc gatcctacga ataacaccag tcttttccgg atgggcaact 660

tctgcacatt tttctaag 678

<210> SEQ ID NO 78
<211> LENGTH: 614
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 78

agttaaatgg tttgggattt aagaaagttt tcttcttata acagagttgg taaatttaaa 60

atacaacgga atataatcga aacaatcagt gaaactatag agatatattg atcacttttc 120

aatttttcat gacccaaaac ctctcaattt ctccagcggt tcttcctggg atcctcccag 180

ctatcagttc ccacctttca tcaaataata acacacaaaa ttcagctttt actatggtgt 240

tacaattaaa ttattttcct acgaaatagt attcattatt agttaaaaga tcaaacctgt 300

caccgacaag cttatgcatt cgagagacca aatcttcttc ttcttgactc atgttcacaa 360

cttcccactc aagactactc acttctgttc cttgtcatca ccaaaattca gatttctcat 420

tatatataga taagtataaa aaaacatgga aaaatgagaa aacgaaggtg tttaagtttt 480

cagcttacct tcagaagaag aagtaacgat ggagttggtc ttgggttgct tagtcctgcg 540

atggttatcc atgtcaaacg gcaccgtatt acaaagaaga agaagaaaga aactaagaga 600

gtactctgag agag 614

<210> SEQ ID NO 79
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 79

gattcgataa gaagaatcta catggctcga catatcatgg agaagttcat cgtcgcagga 60

gcggaaatgg aattgaactt atctcataaa acccgacaag agatcttaac cactcaagat 120

ctaactcaca ctgatctctt caagaacgca ttaaacgaag tcatgcaatt gatcaagatg 180

aacttggtaa gagattactg gtcatccatc tacttcatca agttcaaaga agaagaaagc 240

-continued

tgccacgagg caatgcataa ggaaggatac agtttttcat ctccaagact gagttcagtt 300

caaggctctg atgatccttt ctatcaagaa catatgtcaa agagttccag atgcagtagt 360

cccggttaag gagtctaaaa ctggtactag accagaaccc aaaccaatgt tcatagcaat 420

ccaatccatg taatcttcct tcacatttct tgtacatgtc attttctctc ttgttatacc 480

taactgtaag agaaaatgtc cggttcggat tttggtttag ttttaaatgt gtataccgga 540

caaaaactat ggaaccatac taattaatat ctcgaaga 578

<210> SEQ ID NO 80
<211> LENGTH: 668
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 80

tatagaaatt atgcgtacgc tacaatcaat ggcattacaa tgaaccaacc tggtattcag 60

attttaccaa atgacaatgg acagaaaaaa tatacaattt tgaacagatc agatgcaaaa 120

gttgttctac agacagaaaa agggtaagac ttgatgcatc ttgttgagga gtttgggaag 180

atgatgatga tgatgatcgg taggagtagg tggatctgag ttcttgtctt tctttttttct 240

cctaagctgg aaaaactgct gcattgtctg agcgcattct gattcaagaa ctccgcgccg 300

gattgtcatc ttaggatgga atggatgaac tggaggtggt ggcttttctg aagcctctga 360

tccatttcct tcgcctccag ggaacagcct gatccagctt ccatctgctc cgagaagctt 420

attgggagca ccccatgcaa gagtgttgac ccttgcttga agtattgctc ccgcacacat 480

tgggcacggt tctagtgtta catagagcgt tgtatccgcg agcctccatg aacgaagtgc 540

tttagaaccc tctcgaatgc aaatcatttc tgcatgggca gttgaatcac gaagctcctc 600

tactaggtta taaccacggg caataatctt tccatcatga acaagcacag caccgacagg 660

tacctccc 668

<210> SEQ ID NO 81
<211> LENGTH: 682
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 81

cttcatcaaa tctcacaaat cttcaacact taatcacaaa tctcaaagct tcggatacca 60

aatggctcgt accaagcaaa ccgcaaggaa atccaccgga ggaaaagccc caaggaaaca 120

actcgcaaca aaggcggcga ggaaatcagc tccggcgacc ggaggagtaa agaagccaca 180

cagattccgt cctggaactg ttgccctaag agaaatcagg aagtatcaga agagcactga 240

gcttctgatc cgcaagcttc cgttccagcg tttggttcgt gagatcgctc aggatttcaa 300

aacagatctg cgtttccaga gcagcgccgt cgcagcactt caggaagcgg ctgaagcata 360

cctcgttgga ttgtttgaag acaccaatct ttgcgcgatt catgctaaga gagtcactat 420

catgcctaag gatattcaat tggcgaggag aattagaggc gagagggctt aagaaggaga 480

ttgaagtact ctagactgtg atcgttatgc ttatgtatat ctttcgtttt ccctaatttc 540

gtgttttagg gttggattag gttttgcgtt tatgttgttc gatatctaac ggatcaaaat 600

ctctccttcc ttagcaaagt ttgaaaactc cctccacatt ttcaaaaaaa aaaaaaaaaa 660

aaaaaaaaaa aaaaaaaaaa aa 682

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<210> SEQ ID NO 82
<211> LENGTH: 809
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 82

cgagcttcga cttcgagctg tggaaagtct gccgtgccac gtcagcaaca ccaagcctct 60

tcaagccgtt cagtgtagtg tcggtggacg ggaaaacctc atgctcagcc gtagacggcg 120

gtttggtgat gaacaatcca acagcagctg ccgtcacgca cgtgctacac aacaaacgag 180

atttcccgtc agtaaacggc gtagatgact tgcttgtact gtcgttggga aacggtccgt 240

cgaccatgtc atcatcacca gggaggaaac tccgtcgtaa cggagactat tcaacgtcaa 300

gtgtggtgga catagtggtt gacggcgttt ccgataccgt cgatcagatg ctggggaacg 360

ctttctgctg gaaccgtact gattacgtta gaatccaggc gaacggtttg acgagcggcg 420

gagcggagga gttgctgaaa gagagaggtg tggaaacggc gccgtttggg gtaaaacgga 480

tactaacgga gagtaacgga gaaagaatag agggtttcgt gcaacgtctt gttgcgtcag 540

gaaagtcaag tctacctcca agtccttgca aggaatctgc cgttaaccct ctcgctgacg 600

gccgttaagt ttcctttatt attataaccc tccccgtccg tgatgtaaga agtttgtaac 660

caaacccctg ggttaatttt ttaaccccag ccagcatctt cgagttaatt aattagcctt 720

tctttttttc taatgacttt agttgaggaa ttaataatgg ttaatgaatg atagtcttta 780

cttatttatc caaaaaaaaa aaaaaaaaa 809

<210> SEQ ID NO 83
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 83

tctccttgga atgtccaagc ttgataattc tcttgcttat ctcttcttct cccgctaggg 60

gctctgattc attgtctgcg gacgcgtggg tcgacccggg aattccggac cggtacctgc 120

agccattgga gctctgctgt taattgaaga caagatcaag acaagaggag tcttaaggcc 180

tctcgaagca gaggtgtatt tgccagcttt ggatatattg caagcatatg gtataaagct 240

gatggagaag gcagaatgat caaagaactc tgtatattgt ttctctctat aacttggagt 300

tggagacaaa gctgaagaag acagagacat tagaccagca aaaaaaaaaa aaaaaa 356

<210> SEQ ID NO 84
<211> LENGTH: 1113
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 84

cttcttcagg gttcaggtgt gaaagctgac gccaccgtgg cagctgacgg tagcggtaca 60

tttaaaactg tggctgctgc ggttgccgcg gcccctgaaa atagtaataa gaggtatgtg 120

atacatataa aagccggagt ttacagagag aatgtggagg ttgctaagaa gaaaaagaat 180

ataatgttta tgggagatgg tcggacgaga actattatca ccggaagtcg aaacgttgta 240

gacggtagca ccactttcca ctccgccacc gttgctgctg tcggcgagag attcttagct 300

cgtgacatca ctttccaaaa cacggcgggt ccgtcgaagc accaagcggt ggctctccgt 360

-continued

gtgggttctg atttctccgc cttctacaat tgcgacatgt tagcttatca agacactcta 420

tacgtccact ctaaccgtca attcttcgtc aaatgtctca tcgccggaac cgttgacttc 480

atcttcggaa acgccgccgt cgtgctccaa gactgtgaca tccacgctcg ccgccctaat 540

tccggtcaga aaaacatggt cacagctcag ggaagaacgg atcctaacca gaacacaggg 600

atcgttatcc agaaatgtag gatcggtgcc acgtcggatt tacagtcggt gaaaggtagt 660

tttccgacgt acttgggtcg gccatggaag gaatattcac aaacggtgat aatgcagtcg 720

gctatctccg acgtgatccg acccgaaggg tggtccgagt ggaccgggac ttttgcgttg 780

aacactctga cttacagaga gtattcgaac acaggagcag gggctggaac tgcaaataga 840

gtgaagtgga ggggctttaa ggtaattacg gctgctgctg aagctcaaaa atatacggct 900

ggtcagttta ttggtggtgg aggctggtta tcgtcgaccg gtttcccctt ctcgctcggt 960

ctttgagaga ttgttgtgta atgtgttcct acgtattgtt ggctacaaaa attattgatt 1020

aatattgtat gaagcaaatc gtgttgtcct ctttgttttg tttgggttgt gtactttctc 1080

tagatcatcg tagtattaga aacgagatga aaa 1113

<210> SEQ ID NO 85
<211> LENGTH: 728
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 85

caggcaaaca agaccaagag gaagaagaag aagaaaaaga gaaaaggccc tgtgatggac 60

aaacccatga gtgtagactg gtttgttagg gaaacttgta gacgcctcaa ggagaagaag 120

tcttacatga tatacacagc tgttgggtgt ctcggaattg ctgccttaag tgatcttgtc 180

aatgaggtgg tagcaattga gacctgtgga ggtcaggtga ctgctgatgg cactaggaaa 240

cggacaagtg gtggtgtatt gtggaacatc atcaaagcga gacagcctga agcttataga 300

gagataatga aaaagaccaa ggagtttgag aaacaattta ggcaaccaaa cacgagacca 360

aaatcagggc ccaaaagaga tcagggtagc tcctccgaag gagttgcctc tggaaatgta 420

tctgctgatg aagctctggt gagcgagatg tgtgttatgc cggtagctga ccagactgaa 480

tccaaaccgg aaaaggaaag gaaatctgtt catgagagga tcagggtacc tgtttcatat 540

gatgaccttt tcagagatgc acctttagat gattctctag cacatcattc ttctgcttaa 600

gctcattact ggatgacttc tcttgtggaa agcaattgtt ttgtcgagaa atggaaagca 660

ttgattttgt cgagaaatgc attgacaaaa ctatatatac caactaccaa gatttcttaa 720

atacacaa 728

<210> SEQ ID NO 86
<211> LENGTH: 871
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 86

caagaacatt ctcagcttct agaaggtttt ctcaccaacc cccaaattat gagaaaatta 60

cgaaattggc taaccaacta caaaagaatg attcaattca ccaaacgaat taaatgaagc 120

attaaattga gagtaaatga gttttcgtta gagtgaaact cacgtaagtg ttgagctgac 180

gaatgaagct tgagaaatta ttatgcttga agtattgagg aagaagatct ttagcaaact 240

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ctgctgtttt ccacacgaca aaagctgttc cttcttcgtt ccatgaaacg acgtcgtctg 300

tgctatgatc atcaactagc tgatacgttt tgcttaaaaa cggcgccgga actgatcttt 360

gcgccgccgt cacagccgtc atctccggcg aacttttttt attttaccac agaaaaataa 420

aactaaaaat aatctaatac acaaagagaa gaagaaagat tggaaataga aagtcgaagg 480

aaaaagaatc agcaactaaa aagcaagaga gcggtgagaa attcccaatc ccagcaataa 540

aagccagaga ggaaaacacg agaacggaga agatcggagt ttcgtttggt ttcttccatt 600

taaggaaaaa tctgatgatg gaggaagaag atgaagacga cgaccatact tcgccggagc 660

taatccgtgt gattaaaaag taaataaata taaagtcttt tttatttttg tgtgtatgtg 720

caaaacaagt aaaacaaata tataaacgag ttaagtgtta tgtcgaaggg tctctatata 780

acgtagtagg aagatttata gatcacaaat gttggtccta cctttgtaag aaaattaaat 840

tataaaaacg gatgctgttt ctagaaaaaa a 871

<210> SEQ ID NO 87
<211> LENGTH: 962
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 87

gaagaagttc cgtataacat ctccattatt cagatcagta gagttttacc gtcggagact 60

gcggcggctc cgactcctgc tccggcggag atgaatctta ccggaataat gtcggctcat 120

ggatgcaaag tgtttgctga gactcttctc actaaccctg gagcttcaaa aacctatcag 180

gagagtttag aaggaggcat gacagtgttc tgtccaggag atgatgcaat gaaaggtttc 240

ttgcccaaat acaagaactt gacagctcca aagaaagaag catttctcga tttcctcgct 300

gtcccgacat attactcaat ggcgatgcca aatccaacaa tggtccgatg aacacacttg 360

cgacagatgg agctaacaag tttgagctta ctgtacagaa cgatggagag aaggttaccc 420

tcaagacaag gatcaacact gtcaagatcg ttgatactct tattgatgag cagcctttag 480

ctatatatgc gactgataag gttttgttgc ctaaagagtt gtttaaggct tcggctgttg 540

aagctccggc tcctgctccg gcaccagagg atggtgatgt tgcggattct ccaaaagcgg 600

ctaaagggaa agcgaaagga aagaagaaga aggctgcacc gtcgccagat aatgatcctt 660

ttggtgactc ggattcgcct gccgaagggc ctgacggaga ggccgatgat gcgacggcag 720

atgatgctgg tgcggttagg atcatcggag gagctaaggc tggtttggtg gtgagcttgc 780

tctgcttgtt tgcttcttct tggcttctat agtttcactt cttgtttctt cgattcttcc 840

atgttttttt ttttttgtga atcttttatt tatggttttt gggggagagt aaatgaggat 900

tatttatttc cctctattgt tgagtttttt ttatttattt aaaagttggt tgtcgaatta 960

aa 962

<210> SEQ ID NO 88
<211> LENGTH: 835
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 88

ggacaaggaa ggaatccctc cggatcagca gagacttatc tttgccggta agcagcttga 60

agacggaaga actcttgctg actacaacat tcaaaaggag tcgacccttc atttggtgct 120

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tcgtctcaga ggtggtatgc aaatctttgt caagaccctc actggtaaaa caatcaccct 180

tgaggttgag agttcagaca ccattgacaa tgtcaaagct aagatccaag ataaagaggg 240

aattcctccg gatcagcaga ggcttatctt tgccggtaag cagctcgaag atggacgcac 300

ccttgcagat tacaacatcc aaaaggagtc gacacttcat cttgtgcttc gtctccgtgg 360

tggtatgcag atctttgtga agacccttac cggaaagacc attactctgg aggttgaaag 420

ctcagacacc atcgataatg tcaaggctaa gattcaggac aaggaaggga tcccaccaga 480

ccaacagaga ctcatcttcg ctggaaaaca gcttgaggat ggtcgcacac ttgcagatta 540

caacatccag aaggagtcga ctcttcactt ggttcttcgt cttcgtggtg gaagcttcta 600

agctttttgt gatctgatga taagtggttg gttcgtgtct catgcacttg ggaggtgatc 660

tatttcacct ggtgtagttt gtgtttccgt cagttggaaa aacttatccc tatcgatttc 720

gttttcattt tctgcttttc ttttatgtac cttcgtttgg gcttgtaacg ggcctttgta 780

tttcaactct caataataat ccaagtgcat gttaaacaaa aaaaaaaaaa aaaaa 835

<210> SEQ ID NO 89
<211> LENGTH: 581
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 89

atacaaacac tagaagtctt ataaattcaa agtatgtctg agttttacaa cattagagag 60

aaagagaaca acacagaaac atttatagaa acatgattac acatgcgcta acaactttaa 120

gatttactga gccaaagcac ttgtgttgta cacaagaaga gcacctccgg caagaattcc 180

ggcgagagtt accgcccaaa ttgccaatcc ggtgactcct cccttgtaca cgtcaccact 240

cgctgaccac tcgttctcgt tgtaaatagg actgtatcca tcgacgttag ctccatactt 300

gtcgacgtac ttgtaaacac cgtatccctt gccctttctg ccggaggcgt cgacgccgtc 360

cctcaagtcc atgctgccgt taattccgaa gggcttgtcg gtcttgatct tcttgacgcc 420

actggcgaca attttgaagg agggacgagc tcttgtgagc gacggtaatc ctctagccgc 480

cgtcttctcc accgtgaaac cagctggttt caatgtcacc gaagatagca tcactgaagc 540

agccattatt tttctcacaa gatgatcaaa ctattcttct c 581

<210> SEQ ID NO 90
<211> LENGTH: 884
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 90

tttaatgctt ttctaatcaa taaatatcaa attatccacc agataaaaat aataatttaa 60

aaagcgtatt ctcaaatcgt aacaaaaagg gatatttttg gtgtttgtca cccaaaagta 120

taacctatcc aatgagggta tgaagaaaat tgagtgaatc aaaatataaa agataaaaaa 180

aagggaagac gaagcaaaac tcttttgtat gtttcttctc attagcaaag gctggggtaa 240

aacttagaag ttgacttgaa agccactgcg tctgcgatga cctgcaccgc cttttgatct 300

gtttgagttt ctttcatatt ggtatcgcat ccccaaaccc ttaccgcaag cctacgacat 360

ttgggtgatg attctctgaa ataggttttg taccaactga tcacatcttt cttctgtata 420

cttcttagtt cttctgcttc tttgtgggag aaatcaaaca tgtacctttt gtcaacaatc 480

-continued

tgactccata agtcatttgt ctcggacaag agagagggat ccttttccag caatctagca 540

atcataccac ttcggtaatc ttcataggat tcatcatcca gttgttccag aagcccttcg 600

atatctttta tgaaattgtc aactctcccc agcaaatgaa ctggaccgta cttagaagat 660

tgaacacaga aacagaaacc gtgcacacga tacgttaagc gagggccaca ctcgacaaca 720

taaccaagct gctcctttgt cctcaactga ttgaacaatg gctcttctat gatttcatga 780

aagagatcca gcacagcttt cgttctcgtt gattgagctt cttcaggctc gatttgatag 840

taaagctcga ctactgagtt tgtttcagat ttgttcttca catt 884

<210> SEQ ID NO 91
<211> LENGTH: 730
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 91

gtaggggcaa aacatattat accataagga ccacaaaaca tcacaacaat gatattttca 60

acagagtact agtagagtat gtttataagg agggataggg aatttttttc aaacatagaa 120

cagattctct gagagagaat gttttcataa gagagtatta tatagctaac tctgatttca 180

gcaggtcaag agaggagatg aaccactgca tttgacatca gaagcatcag aaaggcgttg 240

tcttggagag agtgttgtaa tcgctgcaac atctacgtcg agattcacta tgagcttcct 300

cttctgcgac tctgttacac tgttccttct ctcttctgat ccttcagcaa tgggactcaa 360

agtctgtgtc tctgctgctc caacgtcttc tccatctgct gcgtatagga ttctttttat 420

ggaaccaaca agaggtaagt gctctgtgtc tgggttttga cagagaatct ctacatctct 480

gagtttagag aaatagaaat ctctctcttt ctctaagctg tcaatgtaaa gtttcagttc 540

tgtgatcttt tcatcataag caggcactgg tttagattgt ttagctgatg gttttgaaga 600

gtggtggtga ttcccagttg aagaatggtg agtaccggtg ttgttggatt gtggctcatg 660

cttacgggtt ccatttgaag atgaaggtcg aggtggagct gaagaagacg aactcttgcc 720

tgattgttgt 730

<210> SEQ ID NO 92
<211> LENGTH: 1706
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 92

aagaaaagta attctctgtt tgtgtagttt tctttaccgg tgaattttct cttcgttttg 60

tgcttcaaac gtcacccaaa tcaccaagat cgatcaaaat cgaaacttaa cgtttcagaa 120

gatggtgcag taccagagat taatcatcca ccatggaaga aaagaagata agtttagagt 180

ttcttcagca gaggaaagtg gtggaggtgg ttgttgctac tccaagagag ctaaacaaaa 240

gtttcgttgt cttctctttc tctctatcct ctcttgctgt ttcgtcttgt ctccttatta 300

cctcttcggc ttctctactc tctccctcct agattcgttt cgcagagaaa tcgaaggtct 360

tagctcttat gagccagtta ttacccctct gtgctcagaa atctccaatg gaaccatttg 420

ttgtgacaga accggtttga gatctgatat ttgtgtaatg aaaggtgatg ttcgaacaaa 480

ctctgcttct tcctcaatct tcctcttcac ctcctccacc aataacaaca caaaaccgga 540

aaagatcaaa ccttacacta gaaaatggga gactagtgtg atggacaccg ttcaagaact 600

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caacctcatc accaaagatt ccaacaaatc ttcagatcgt gtatgcgatg tgtaccatga 660

tgttcctgct gtgttcttct ccactggtgg atacaccggt aacgtatacc acgagtttaa 720

cgacgggatt atccctttgt ttataacttc acagcattac aacaaaaaag ttgtgtttgt 780

gatcgtcgag tatcatgact ggtgggagat gaagtatgga gatgtcgttt cgcagctctc 840

ggattatcct ctggttgatt tcaatggaga tacgagaaca cattgtttca aagaagcaac 900

cgttggatta cgtattcacg acgagttaac tgtgaattct tctttggtca ttgggaatca 960

aaccattgtt gacttcagaa acgttttgga taggggttac tcgcatcgta tccaaagctt 1020

gactcaggag gaaacagagg cgaacgtgac cgcactcgat ttcaagaaga agccaaaact 1080

ggtgattctt tcaagaaacg ggtcatcaag ggcgatatta aacgagaatc ttctcgtgga 1140

gctagcagag aaaacagggt tcaatgtgga ggttctaaga ccacaaaaga caacggaaat 1200

ggccaagatt tatcgttcgt tgaacacgag cgatgtaatg atcggtgtac atggagcagc 1260

aatgactcat ttccttttct tgaaaccgaa aaccgttttc attcagatca tcccattagg 1320

gacggactgg gcggcagaga catattatgg agaaccggcg aagaagctag gattgaagta 1380

cgttggttac aagattgcgc cgaaagagag ctctttgtat gaagaatatg ggaaagatga 1440

ccctgtaatc cgagatccgg atagtctaaa cgacaaagga tgggaatata cgaagaaaat 1500

ctatctacaa ggacagaacg tgaagcttga cttgagaaga ttcagagaaa cgttaactcg 1560

ttcgtatgat ttctccatta gaaggagatt tagagaagat tacttgttac atagagaaga 1620

ttaagaatcg tgtgatattt tttttgtaaa gttttgaatg acaattaaat ttatttattt 1680

tattaagttt tttttggtaa aaaaaa 1706

<210> SEQ ID NO 93
<211> LENGTH: 737
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 93

agaagaagtt aaagcaaaac acatacaaac gcagtcacct tctctgtcgc ctccttcttc 60

aatctcatcg caatcatgat catatccgag actaatcgcc gtgagatctc caagtacctc 120

ttcaaagagg gtgttttgtt tgccaaaaag gatttcaatt taccacaaca tcctttgatt 180

gagagtgttc caaatctgca agttatcaag ttgatgcaga gtttcaaatc taaggaatat 240

gtgagagaga cctttgcttg gatgcattac tactggttcc tcacaaatga aggtattgac 300

tttcttagga cttaccttaa tctcccatct gagattgttc ctgctactct gaagaagcaa 360

cagaagcctc ttggtcgacc ttttggaggt ggtggtgacc gtccccgtgg ccctcctcgt 420

ggtgatggag agaggaggtt tggtgacaga gatggatacc gtggaggtcc taaatcaggt 480

ggagagtatg gtgacaaggc tggagcacct gctgattacc agcctggctt caggggtgga 540

gctagtggag caaggcaagg gtttggtcgt ggagctggtg gttttggtgg tggtgctggt 600

ccagctgctg gatctgatct accttgaaaa ggactttctt gtttcttttt ggtcttattt 660

aaggttacat agcaccttat tgagaacgaa tgtgtctttt ggaactttgt ttctttctct 720

taaaccattt cacaaaa 737

<210> SEQ ID NO 94
<211> LENGTH: 907

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<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 94

agaaaaagaa caaaaaccta atttcaagaa attcaataaa tatcatcctc cggataagtt 60

gttattgtac gtttaccaaa ttcaagaaca agaaaaaact tttcctttga aacaaagaaa 120

catggatttc ttcaccgatc aagtaaagaa gaaattctcc gacaagaaac cggagagctc 180

tgatccggag ccaaaccaca acaaaaacaa acccggtcac acggagccaa caacacataa 240

acccggtcac ggcgagccaa caacacataa accggtctcc aacaccgatc caacaacaca 300

cagaccggct acgaacgctg agctcatggc tagtgccaag atcgtagccg aagctgctca 360

agccgctgct cgtcacgagt cagacaagct tgacaaagcc aaagtcgccg gagccaccgc 420

tgatatctta gacgccgctt ctagatacgg taagctcgat gaaaagagcg gtgttggtca 480

gtaccttgaa aaggctgaac aatatcttca caagtacgaa acttcccact ctcactcctc 540

caccggtgga actggaagcc acggtaatgt tggaggacac ggtggtggag ctggagcacc 600

ggcggctaag aaagaagatg agaagtccgg aggtggtcat gggtttggag attatgctaa 660

gatggctcaa ggtttttatga agtgagtaat gttttagttt ctaaaaataa ttatgttagt 720

aattatcttc tataattact gttttagtaa gctgttgttt tttctgaatt attattaact 780

gttggatttg tcatttgtgt atgatggagg aaattatgat gttaaagatc atgtatcatg 840

ttgttgacca ctcgagattg cgttaatcaa atatttgtat aattagaacc gaactttaag 900

ttaaaaa 907

<210> SEQ ID NO 95
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 95

atacaaggaa agtgttttgc catctgatgt atcagctaga gttagtatcg aagctggatc 60

gacttttgga tggggaaaga tcgtcggagg aaaagggaaa tcgattggaa ttgatacgtt 120

tggagcaagt gcaccagcag gaaagcttta taaagagttt ggtatcacca ttgaagctat 180

ggttgaagca gccaagtcac ttatttaaaa aagtatctta caggtactac cgaggtttgc 240

atttgaagta agagacattc cataagcatt atcttctttg tccaaataaa aatatactcc 300

ttccaatctt tttataaatg atgtttaaag ctttcatttt ggtttttaaa taaatgatgt 360

tttaaatttt caatgcaaaa ttatttttat tggttgatta aataaatgat gttttaggct 420

tttatttata ttttaaa 437

<210> SEQ ID NO 96
<211> LENGTH: 413
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 96

cttgtcaaag agaagtgtgt ttgcgtcatc ttcgattagt gtggggaaaa acttggagga 60

tatgtcagcg tatattcatt tcttggcgtc tggatttgaa gcttccagaa cagcttttgg 120

tgctatacct ggaagcttgc agcccgatga agagttatgt agagatcttg gtttgtctct 180

caacactcct tccccaaata ctcgcaagca agattgacct gtttttttaat ttatctttgt 240

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ctgcatatca ttgggatatt tttgtgtata aatcaatgta tactatctga atcattctat 300

agcagctttg gtgtaatatt gatgatgaaa gttagatttt tcatctaaaa aaaaaaaaaa 360

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 413

<210> SEQ ID NO 97
<211> LENGTH: 1365
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 97

ttttttttt taagaagaag ttcgacttgt cattagaaag aaagagataa caggaacgga 60

aacatagtag aacacttatt catcagggat tatacaaggc cccaaaacac aaaccaccaa 120

agttttacat gaaacgaaac attgaacttc ttaagcataa cagagacgag atttagaaac 180

caccacgaag acgcaggacc aagtgaagag tagactcctt ctggatgttg tagtcggcca 240

aagtacgtcc atcctcaagc tgctttccag cgaagatgag acgctgctgg tccggaggaa 300

taccttcctt gtcctggatc ttggccttga cgttgtcaat ggtgtcggag ctttccactt 360

caagggtgat ggtctttccg gtcaaagtct tgacgaagat ctgcatacct ccacgcagac 420

gcaacaccaa gtgaagggtc gactccttct ggatgttgta atccgccaaa gtacgaccat 480

cctccaattg ttttccggca aagatcaacc tctgctggtc cggagggatt ccttccttat 540

cctggatctt ggccttcacg ttgtcaatgg tgtcagagct ctctacctcc aaagtgatag 600

tctttccggt gagagtcttc acgaagatct gcatacctcc acgcagacgc aagaccaagt 660

gaagtgtgga ctccttctga atgttgtagt cggccaaagt tcttccatct tcaagttgct 720

ttccggcgaa gatcaatctc tgctggtccg gaggaatacc ctctttgtcc tggatcttgg 780

ctttcacgtt atcaatggtg tcagaactct ccacctccaa agtgatagtt ttcccagtca 840

acgtcttaac gaaaatctgc ataccaccac ggagcctgag aacaagatga agggtggact 900

ccttctggat attgtagtca gcaagagttc tgccatcctc caactgcttt ccggcgaaga 960

tcagcctctg ctggtccgga ggaataccct ctttgtcttg gatcttggcc ttgacgttgt 1020

cgatggtgtc agaactctcc acctcaagag taatcgtctt tcccgttagg gttttaacga 1080

aaatctgcat accaccacgg agcctgagga ccaagtggag ggtggattcc ttctggatat 1140

tgtaatcagc caacgtacgg ccatcctcta gctgcttgcc ggcgaaaata agcctctgct 1200

gatccggagg aatgccctcc ttatcctgga tcttggcctt aacgttgtcg atggtgtcgg 1260

agctttccac ctcgagggtg attgtctttc cggtgagagt cttaacaaag atctgcatct 1320

tgatcacggt agagagaatt gagagaaagt ttttaagatt ttgag 1365

<210> SEQ ID NO 98
<211> LENGTH: 878
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 98

cgtttgtttg caactcttga tccaactacg agaagggttc agatgcaaaa cgggaaggaa 60

tttcttctca cagatactgt tggttttatc caaaagttac caaccactct ggttgctgct 120

ttcagagcaa cacttgaaga aatagcagag tcaagccttt tggtgcatgt tgttgacatc 180

agccacccac tggcagagca acaaatagaa gctgtggaga aggttatgtc tgaactcgac 240

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gtttcatcaa ttccaaaatt ggtcgtgtgg aataaggttg atagagtgga tgatcctcaa 300

aacgtcaagc tggaagcaga ggaaactggg gatacaattt gtatatctgc tctgactgga 360

gaaggactag acgacttctg caatgctgtt catgagaagc tcaaggattc aatggtttgg 420

gttgaagccc ttttgccatt tgataaaggg gaccttctaa gcaccataca caaggttgga 480

atggtgaaag aaactgaata tacagagaat gggacactta tcagggcaca cgttccgcta 540

cgttttgcac agctgcttaa acctatgaga cacttggtca aagatacttc aataagccaa 600

agaggatgaa ccagaatcat agcaagaacc tgaaggcctg cctcttggtg agaatcggag 660

gctacgtgtg ctttgccaaa gcatccgaaa gcaaaaggaa ttcaaacaac cttctgatca 720

tacacaccac aaagaatgac agtcagacag taaagaatat tcgtagataa aaaggaatgc 780

agctagacac aagcaagata agcttgaacc tacttcacat cgtgaactga cactggaaat 840

gttatttcaa cagtgataag tgataaccct ttttgtaa 878

<210> SEQ ID NO 99
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 99

aacataacat taaactgctt tcacatagaa agcaaaagtc ttaaacaaca ttacattaac 60

tcctttcaca taaacagaaa agtcttaaac aacattacat aaactccttt cacacagaca 120

caaaaggctc tttcttgctc aacgcatcaa cactcttagt tcaagatttc acctgtaatg 180

ggtgaaacat gttggctcgt agacttctgc ccatttttg aaccgaccac taccataggc 240

tttggtggta tcaaaccggc cctgaaaagc atgctttcca ctgtgtctgt tggttgagct 300

ccaacagata accagtactt gattctgtcg aatttgaggc tcactctatc cgcatcttct 360

ttgccttgga gtggatcata aaagcctaac acctcgattt gtttaccgtc cctgcgcgat 420

ttttcatcgg cgacaactac acgatagaag ggtcggtgtt tacaaccaag acgcgc 476

<210> SEQ ID NO 100
<211> LENGTH: 713
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 100

gattatgccc ctctcgtcac caaggccaag ggccgtaaac tcacggctga ggaactctgg 60

tcagagctcg atgcttccgc cgccgacgac ttctggggtt tctattccac ctccaaactc 120

catcccacca accaagttaa cgtgaaagag gaggcagtga agaaggagca ggcaacagag 180

ccggggaaac ggaggaagag gaagaatgtt tatagaggga tacgtaagcg tccatgggga 240

aaatgggcgg ctgagattcg agatccacga aaaggtgtta gagtttggct tggtacgttc 300

aacacggcgg aggaagctgc catggcttat gatgttgcgg ccaagcagat ccgtggtgat 360

aaagccaagc tcaacttccc agatctgcac catcctcctc ctcctaatta tactcctccg 420

ccgtcatcgc cacgatcaac cgatcagcct ccggcgaaga aggtctgcgt tgtctctcag 480

agtgagagcg agttaagtca gccgagtttc ccggtggagt gtataggatt tggaaatggg 540

gacgagtttc agaacctgag ttacggattt gagccggatt atgatctgaa acagcagata 600

tcgagcttgg aatcgttcct tgagctggac ggtaacacgg cggagcaacc gagtcagctt 660

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gatgagtccg tttccgaggt ggatatgtgg atgcttgatg atgtcattgc gcg 713

<210> SEQ ID NO 101
<211> LENGTH: 1094
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 101

aaatcagtga gaaggtgcaa gtcgctcaca agagaagaaa tcgacacttt ttggaaaacg 60

aagaagaaga atgaagaaga agaacatgtt caagcctttt ccaagttggt aactcaggaa 120

ggtgcacaaa gccaagcgaa agagaagaag agtgtagatg atctttttga gaaccaaagc 180

aagagtagtg gatggtggag aaaaacctac tgggcgttct tgaatgagcc gagggaggaa 240

gagggtcgac cgaacaacta cgtgtcgcaa ttcaaagttg ctcacatcgc caaaattgcg 300

ggctcgtaat gacgctataa tcaccggcta atcacatata tatctcgtgt gaaatgcgat 360

tagtcgtctg ccgttgtggt ttaatcaccg gctaatcaca tatatagtat gttggccgtg 420

ttagtatgtg aatgtgtgag tagagcatgt aacaaagggt gtacgatttt aatgtaagaa 480

tgtgttttac tttatatgtg tcatgtatgt atttttttgg ttgtgtgagg gtgtaatgcg 540

gccgcaaaaa tatcattcat agggccactc tcatttttt taggatttag aacaaaatcc 600

gaaaaggagt gacataacat tacaacatta ggaataaagt agataaaaca ttgatcaaag 660

gaaatttagt tatagttgaa aatttttatt ataaaaaggg aacgaaggga gatttttca 720

agggcatttt ggtccaccct cttgagtttt ccagttgttg tagcaggagc aaacttgttt 780

gttcccatag taacccggag gcacacagag acacttcctg cagcatttgt tgcagaacgt 840

aatgcaagcc ttgtggtact gtgtcttttt acacctccta tcacattccg atgggcattg 900

ggtacgtttc aggcttcctg gtccataacg tttctggctc cacttcacat tagatccact 960

tgaggccata accatggttt gaagcatgaa gaggacaatg agggtcaaga ggaagatagc 1020

tccatatgac ttagccattt tcagtttggg atattgttat ccaaagaacc aaacactcct 1080

ctaaatctcc cgcg 1094

<210> SEQ ID NO 102
<211> LENGTH: 663
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 102

gcaacatacg tcttttctaa atcattacat ttgaagaaga gaaacaaaaa cagagcggaa 60

tgccgaattt gtttctcttc tcgattcaac catccgaaaa caagaataca aaaagagaag 120

ataatcgcgg aaacagatta cgtaatagaa gcttgagttg ttttgtttct atttcttttc 180

gagaaagctc cgaacttcag catctgaggg aagagctgga atggctcctt ttttggtcgt 240

tgtgattgct ccacaagcat ttgcgaatct cagcactttc ctcaatctct cttcgtcctc 300

gagaacggat cgatcatcga caatctggtt tagaagagca ccgacaaagg aatctccagc 360

tccggttgtg tccacagcgt tcacatggaa agggtcaacg gctcctttga aagtcttggt 420

gtaataccga cagccctttt caccaagagt gactaacaac agcttcaagt tgggatgcca 480

caaggtcaac gcggtctcat catcaatctt gttgcttcca gttagaaact caagctcaac 540

atcgctcacc ttgatgatct cagctttgtc ccaaatgctc atgatctgtg ttttggcttc 600

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ttcttttgat ggccacagag gctccctgag gtttgggtca taggaaagaa gagctcctgc 660

gcg 663

<210> SEQ ID NO 103
<211> LENGTH: 688
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 103

aagcgaagag tctgaaagcg actaaatgta cattataaag aaacagattt tgattttgaa 60

agatctagta acaaaaacaa atttccgtta tccccatgtt cttatgcagc catgggcaca 120

gcttctgatg gtgctgcagc agctgcgtct gggacgtacc aaccatggtg aatttcaacg 180

gctttttcc tcctagccaa tcgagacttc ctacgggcac cagtgttctt gtgtagtgct 240

ttaaccttca ctgctttgtc aattgcagaa taagcctctc ctatcagttt ctccaccgtc 300

acaatctcat cagcttgcgc atcagttttc ttcttgagcc cctcaagtgc ttccaagacc 360

ttcttcatcc gggtacgggc ttcagatttc ttagatttgt tgtaaacacg cctcttctca 420

gcttggcgag ctctctttgc agctgaatca gctttcttgg taggagcagc agcctcacac 480

acaatcaatt gcctcattgg cttctgtacc cacaaattcc cggttgagaa ggcgacgcat 540

tgagaaacgc tctgagagaa gctaagggaa gaggataagg tagccgaagc accacgacga 600

ttggagaagg aagaagatgg tgacgaacaa gagattccct taagcgaaag gactttgaat 660

tgggattcga gggtcgcaca ggaagaaa 688

<210> SEQ ID NO 104
<211> LENGTH: 1111
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 104

gtcttcttat gattaccctc tcttccctaa ttacatggct aatactcagt cttctaaagc 60

caaggctcgg tctcaaagtg cgccgaagca gagacctcct gagatctatg agaagcagat 120

gagtgggagg agaagatctt cgatggaagc accgaggaat aacggtgtcc cgagagctgt 180

aaggatgcag agatcttcat ctcaactagg gtcaaacaca gccaaggaaa gtcaacaaca 240

tcatcatcat cagtactatc cgtggatggc gataaagctc gatagatcta atatttcgct 300

tatggagagc gaatgcggat ctacaagtac cgttatgact aataccaact acggtagaca 360

tgttgatgtt cagggaaaca acaacatgta ctgaacactg tgctttagaa tttgagagat 420

tgctggaaaa ataggcaagc ctaaaaaacg aagaggacag gtttatagga gttttttta 480

tgatgatgga gatttaacaa tctctatatg taaagcaaaa aatgtagtag actgtagaag 540

tgactcatct cgtcttaaat tttgattttt ccttttaat tatcattcga attaacgtta 600

agcggccgcg ctatcacaca ccttggaaga aaacgaagta ttccctgcgc agtttggacg 660

ggaggttcta gcagggttgc taaagatccc agatagggcc gattggagaa actgtaaaat 720

tagccaagaa gaggaggcaa agctggctga agatttcaag aaacaatttc aagaatttga 780

cccttgccaa taaccttact gaacaaaaga tacgattaga tgctatcttg tgggcatcaa 840

tcatgctaaa ctcagtctcc agtgcactca ggtcagaagc tgaatcatgc gaagcatcgt 900

cgtttagaaa taggtttgtc aacagtgttc tttgtttggt cagttaaaag ctaacagtct 960

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tccatcagtt tccttactat tttactggtt agttgttacc tatcttgttc ttctattaaa 1020

catttttttt gatatattat tgtttgttga gatgtaagag agtgatcatc acagaaacac 1080

acaacagtca tggtagaatt tgcttcacgc g 1111

<210> SEQ ID NO 105
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 105

tgcatgttcc ctaagttaac agaggagaca aaagatgatg ataagttaca ttttagaaca 60

caaccatatt tcctcttcag actcgccaca caaacctcta taagcgagag aaagaagctg 120

aaaaaaacca ctctctttct ttatttagta agagttttgc cagagctgct gctgagattg 180

attcgacggt tgaccagcct gagacccagc accatcccta gggttttgct gctggcgctc 240

gagtgacatt tcggtctgag actgataata atttgggtat ccatgagatc cataatgctg 300

ttgttgctga gcttggcgat accctcccgc tgcttgctga gcctgctgtt gttgttgctg 360

gtgttgtagt tgcagttgtt gttgtgcttg gaggttgtaa tacgtgttag tcgggacacc 420

tgacatggtt ctggaaccat gaccctgatg ccacatcgcc gagttttcgt tctgttgttg 480

atgttgctgt tgttgctgct gctgctgaag tgccaacaga tgattctctt tgtattgaga 540

actaagaaca tcgtcataac caagcgttgt accggtagta gcagactgtt ggttaagagg 600

gaagtttccg cg 612

<210> SEQ ID NO 106
<211> LENGTH: 703
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 106

actgagttcg ataggatact attgttcgaa caaattcgtc aagacgccga aaatacctac 60

aagtcaaatc ctttagatgc cgataatctg actagatggg gaggagtttt actcgagtta 120

tctcagtttc atagcatctc agatgcaaag caaatgattc aagaggccat cacaaagttt 180

gaagaggcat tgttgattga cccaaagaaa gatgaagcgg tttggtgtat tgggaatgca 240

tacacttcat ttgcgtttct gactcctgac gagactgaag ctaaacataa ctttgactta 300

gctactcagt tctttcaaca agctgtggat gagcaaccag ataatacaca ctacctgaaa 360

tcactcgaaa tgacggccaa ggctccacag ctgcacgcag aagcttacaa acaaggctta 420

ggctcacaac caatgggtcg cgttgaagct ccagcaccgc cgagctcaaa ggcagtgaag 480

aataagaaaa gtagtgatgc caagtatgat gctatgggtt gggtgattct agccattggt 540

gttgttgctt ggatcagttt cgcgaaagct aatgtgcctg tctctcctcc tcgttaagta 600

gactcgttag gagactttga tgaagttttt caatttttga ggttttgaca gttggagctt 660

gttgtgtaag atttttagtt gtactacgag tactttatta gcg 703

<210> SEQ ID NO 107
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 107

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gggacgtcaa ggagagagag ttagattgta tgttcgtgga acagtcctcg gttacaagag 60

gtccaagtcg aaccaatacc ctaacacttc tctcgtccag attgaaggtg tgaacactca 120

agaggaggtt aattggtaca agggtaagcg tttggcttac atctacaagg caaagacaaa 180

gaagaacggt tctcactacc gttgcatttg gggcaaagtc actaggcctc atggtaacag 240

tggtgttgtc cgttctaagt tcacttcaaa cctaccaccc aagtcaatgg gagctagagt 300

cagagtcttc atgtacccta gcaacatatg aggaggctag atttcaacaa gtatcggaag 360

gaatcgccat tatcatttct caggagctgt agttttatct attcactttt attctagact 420

ctctgttggt tttgatttta tcttgagacg aagtaaaaca tttttttttct tgagatcata 480

tactatcgag tattaatgga acttgagaaa agcg 514

<210> SEQ ID NO 108
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 108

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attctttgtt tcctcagcta agttagcaat agatgacata tcttgctgcg cctggaaaga 120

aattcggttg atgagatcgc ttgcagtgat atcgatgttg gaatcatctg gtccgtggcc 180

aaaaagatca gaacttgaaa tagctgctga acccgagaac ttctgaaggg tagcttttga 240

gtcaagatcg gcatctctgt tctgatttcc gaaaaattgg gcagaggaaa tcgatttggc 300

gtttgaaaac ttctttcttg cttcatctgt ttcttcaacc tgagctttgg atgagcttga 360

gcttgacttc ttggggaaag cactgtccat tccaaattca ttaaagaaat ttgatgactt 420

tggtggagca acatggctaa gcacccgtgt gccactttgc ccaccagatt gctcatcatc 480

aaagtactca aatcgagagg caaatgatga tccagctgct gatgtgtcat tggttggaga 540

agcagcagga atcacaggta caggttcttc aggcttctgc tcatagaggt tatcctttga 600

cttagtagta agcttacgag caccaagacc accagtcttc ccagactttc gcgaaacaag 660

aggtttctta aacgtactag caacaacttt ctgagaagct tttggtgaag agacaacagc 720

tgcttcttgc ttcaaagaac tctctttcgg agattcagaa gtaaacccat tttcagatga 780

ttccactggc tgagaagcgc g 801

<210> SEQ ID NO 109
<211> LENGTH: 745
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 109

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catgttggtg taccaagatc ttctcaccgg tgatgagctt ctgtctgact ctttccctta 120

caaggagatt gagaatggaa tcctctggga agtagaagga aagtgggtta ctgtgggagc 180

tgtagatgtt aacattggtg ccaatccatc tgctgaagaa ggtggtgagg atgaaggtgt 240

tgatgactct actcaaaagg ttgttgacat tgtcgacacc ttcagacttc aggagcaacc 300

aacttatgac aagaagggat tcatcgctta cattaagaaa tacattaagc ttttgacacc 360

caagctcagc gaagaagatc aagctgtctt caagaagggt attgagggag ctaccaagtt 420

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tttgctcccc aggctcagtg acttccaatt ctttgttggg gagggtatgc atgatgacag 480

cactttggtc tttgcttact acaaggaggg ttcaactaac ccaacatttt tgtacttcgc 540

tcatggtttg aaggaggtca agtgctgaga gagaagctct cgttgggtta ctgtggtcgg 600

tcgcagcgac tctctaagtt tatgtttctt tatattgtcc tgtgtttcgt cgtcgtcccc 660

tattaaaatt acctgccagt ttacttttct ctcttcttgt tttctgtgtt ggaagattct 720

caagttattt attccgcaaa aagcg 745

<210> SEQ ID NO 110
<211> LENGTH: 572
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 110

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ctctcttctc tttcttcttc ttcttcctcg cgccttcttc aatctccgtc tttcgcttct 120

ccagttttga gccttaaacc caacgctgtc gagtccaaga acagagtctc tctcagtgct 180

tacagcttga actctagcca tggaagaatt gtggtgaagg cggctgcttc tggcgtggac 240

ggggctgagc ctgagagcaa ggaggaacca aagactgttg ttgctgctgt tccagtggat 300

aaactaccgt tggaatcgaa agaagctaaa gagaaactgc tcttggaatt gaggctgaag 360

atgaagctgg ccaaaaagat taggctacgc aggaaacgtc tggttcgtaa gcgtaagatg 420

aggaagaagg gtcgatggcc accttccaag atgaagaaaa acaagaatgt ctaagtgact 480

caactgtttg ctgcttttcg tattcgtttt ttgtaatgtt ctttttggtg ttcaaagacc 540

attaatgtac ttcaaatgca accattgttt tt 572

<210> SEQ ID NO 111
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 111

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gccaaagaat ggaaaggact tcgtgtcacc gtgaagctga cggttcagaa tcgtcaagct 180

aaggtaaccg tggttccatc tgctgcagct ctcgtcatca aggcgttgaa ggagccagag 240

agagaccgta agaaggtgaa gaacattaag cataacggta acatctcttt cgatgatgtg 300

actgagattg ctaggattat gaggcctaga tctattgcta aggagctgag tgggactgtg 360

agggagattc ttggaacgtg tgtctctgtg ggatgcactg ttgatgggaa agaccctaag 420

gatcttcagc aggagattca agaaggtgag attgagattc ctgagaatta aggaacaatg 480

gagtttttt ttcttcttat gggaatttga aatgcttctg ttgttatctt tctcgtttta 540

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<210> SEQ ID NO 112
<211> LENGTH: 815
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 112

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tgaggcagct tttgcctaga cagagctaag atagatggtg tcttgcgctt ggtgacagcg 180

atcttgtatg caccggctgc ggaggtgctc aggaaagacg gcaaaaccgt tagagttgtt 240

tctttcgtgt gctgggaact atttgacgag caatcagatg aatacaagga gagtgtgttg 300

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cccttactct acaaggagtt tggtatcacc gttgaagctg ttgttgatgc ggccaagtca 480

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tttggaaaca aggctattca caacattgtc tcatatctcg aaataaagtg caacaagaca 600

caaagacttt cactttcttt tttgtttttg ttttttgtac ttcaggtcaa gataggtttt 660

cggtttgaga agagaaacaa attagaaaga caatgtaaaa ctcccatgat cattcgtgta 720

atgctaaatg cttgaatttc agcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 815

<210> SEQ ID NO 113
<211> LENGTH: 1106
<212> TYPE: DNA
<213> ORGANISM: Nicotiana benthamiana

<400> SEQUENCE: 113

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taacgttgca gttggtatag caagattagg aggttcttcc gcctttattg gcaaggtggg 180

tgcagatgaa tttggttata tgttatctga tatattaaaa cagaaccatg tcgacaattc 240

tggcatgcgt ttcgataccc atgcaaggac agcattagca tttgtcactt tgagagcaga 300

tggcgagaga gaattcatgt ttttccgcaa tccaagtgct gatatgcttc ttacaaagga 360

agagctggac aaagatctca ttcagaaggc aagaatattt cactatgggt caatctcttt 420

aatcgcggaa ccgtgtaggt cagctcatct tgcagccatg gagattgcca aaaaagctgg 480

ctgcattctc tcttatgacc caaatctaag gttgcccttа tggccatccg cagatgctgc 540

tcgtaaaggc atcttgagca tttgggacca agccgacgtt attaaggtaa gcgaagacga 600

aatcacattc ttgacagacg gtgaagacgc ctacgatgac aatgtggtga tgactaagct 660

tttccaccca aaccttaagc ttttgctggt taccgaaggg ggagaaggtt gcagatacta 720

tactaagaat tttcacggga gagtgaatgg cattaaagta acagcagttg ataccacagg 780

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tgtgacagaa aaaggagcaa ttcctgcatt gccaacaaaa gcagcagtgc ttaaaatctt 960

ggatggtgcc acagctaact gatccaatca aattcccccc acccacagaa aagcctccta 1020

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<210> SEQ ID NO 114
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<212> TYPE: DNA
<213> ORGANISM: Nicotiana benthamiana

<400> SEQUENCE: 114

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gatttcgtgc cgacggtctc cggcgtttcc cttgccgagg ctccgggttt cttgaaggct 180

cctggcggtg caccggcaaa cgtcgccatc gcagtgacta ggctcggggg aaagtcggcg 240

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aacggcgttc aagccgacgg gatcaacttc gacaagggag cgagaacggc attggcattc 360

gtgaccctac gcgccgacgg agagcgtgag ttcatgttct acaggaatcc cagtgctgat 420

atgttgctca ctcccgacga gttgaatctt gatgttatta gatctgctaa ggtgttccac 480

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ccgtcggcag aggaggcgag gaagcaaatc aagagcatct gggacgaggc agatgtgatc 660

aaggtgagtg atgtggagct ggaattccta accggaagtg acaagattga tgacgaatct 720

gccatgtcct tatggcatcc taatttgaag ctcctcttgg tcaccctcgg tgagaaaggc 780

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gacaccaccg gagctggtga ttcttttgtt ggtgcccttc taaccaagat tgttgatgac 900

caatccattc ttgaggatga agcaagactg aaggaagtac taaggtttgc atgtgcatgt 960

ggagccatca caacaaccaa gaaaggagca atcccagctc ttcctactga atctgaagcc 1020

ctcactatgc tttacggagg agcataggac gaagatgatg ttacccttt aattcttttt 1080

aatcgtgata tatttcgacc gtttacgagt ttttcctttc aatcaatcaa aatagtttca 1140

gcctttcatt tcacttttgg ggtttcggat tttaatggtt tcttgtaatg atgaaagact 1200

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<210> SEQ ID NO 115
<211> LENGTH: 803
<212> TYPE: DNA
<213> ORGANISM: Nicotiana benthamiana

<400> SEQUENCE: 115

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tcggaaatga gaccgaagca agaaccttct caaaagtaca tggatgggag actgataatg 180

ttgaagaaat agctctgaaa atatctgaat ggccaaaggc atctgaaaca cacaaaagga 240

tcactgttat tacacaaggt gctgatcctg ttgttgttgc tgagaatggg aaggtgaagt 300

tgttccctgt aataccgttg ccaaaagaga aacttgttga caccaatggt gctggggatg 360

catttgttgg gggattcttg tcacaattgg ttcaaggaaa acctgttgaa gattgtgtaa 420

gagcaggatg ttatgcgtca aatgttatca tccaaaggtc gggttgcaca taccctgaga 480

aaccagattt tgcataagat aagttcttat tcttggtttc tagttttatg ttgacagaac 540

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atattcgact tctagtattt agtactcggt cgagtaattc caatttttgg gctattgttc 600

ccaaaattct acccatgttg taaggaattt tgattgccct tacattattt gagatttgag 660

aataacattg tactagaaaa tttagaaaat ttcttccaat ttctgggcta ttgttcccat 720

ttgtaaggaa ttttgactgt tttttcatat cattcgagaa taacattgta ttaggaaata 780

aaaaaaaaaa aaaaaaaaaa aaa 803

<210> SEQ ID NO 116
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<212> TYPE: DNA
<213> ORGANISM: Nicotiana benthamiana

<400> SEQUENCE: 116

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tgggagaaat atgtcggatc aaaggggaag gccatcggaa ttgatagatg gggtgccagt 180

gcccctgctg gaaaaatata ccaggagtac ggaattacag cagaggctgt tgtagctgca 240

gctaaacaag tttcttaggc tttattactt acacttggtt gctggtgtct accaaatttg 300

ttttcagttt gacactgagg ttggaggtga tggtggaaac caataccaaa cggactcggc 360

agttcactgt tgcctggtat tttcaataaa aactatttct tcatctgccc tttgttttct 420

tcagttttag tagcggagcg gccaaaatga atccaagatg aggatagaaa taggattatg 480

gatgctcctg accatgtaca ctttaaacca tatctttgag ttttgtaatt tcatttggtc 540

gagtgatacc aagatcttat tttca 565

<210> SEQ ID NO 117
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Oryza japonica

<400> SEQUENCE: 117

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ctttatctgt gagtttttcc gtgatgccca ggagaaggtt cttccgtttg tggactacat 180

cttcggtaac gaaacagaag caagaatctt tgctaaagtc cgtggatggg agactgagaa 240

tgttgaggag atcgcgttga agatttccca gcttccattg gcctctggaa aacaaaagag 300

gattgccgtg attactcaag gtgctgatcc agtagttgtc gctgaggatg gacaggtgaa 360

aacattccct gtgatcctac tgccaaagga gaagcttgtt gacaccaatg gcgctggtga 420

tgcctttgtt ggaggcttcc tctcacaatt ggttcaacaa aagagcattg aggactctgt 480

gaaggctggt tgctatgccg caaatgttat catccagcgt tctggctgca cttaccctga 540

gaagcctgat ttcaactagg gctaacccaa ccacatattg aggaacaatt attcgcacat 600

ccaacctact agtggtttgg tgtgttctac ctgtaccatc tcgaggcttt ccatatgatc 660

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gtataaggca caattgccaa tcggtgtgtt gttttggtc 759

<210> SEQ ID NO 118
<211> LENGTH: 630

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<212> TYPE: DNA
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<400> SEQUENCE: 118

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atgaacagtc ggctgagtac aaggagagtg ttctccctga ggctgttact gcaagagtca 180

gccttgaagc agggtctact cttggatggc agaagtacgt cggaagcaaa ggcaaggcta 240

ttggcatcga caaattcggt gcaagtgctc ctgctggaaa gatctaccag gagtatggca 300

tcaccgcgga gaacgtcatc gcaacagcaa agagcctgta agattcaaac cgcgcgtttt 360

gagtttttgt catcgttgat gccaaggaac agtatacatg aagccatgaa ggtcttgtgc 420

ccaaagcttg gaataatgaa gggagaggga tgcctgcatt ggagcgtgag tggtatttta 480

ggcctgtaat aagcactgct tttccattta cgtttgtttt gttggatcac tccttagatg 540

attcatcaag ttgagcctga ttcaattggg gactggtttt ggtaatattt acatttgact 600

atagtccagc tacaatattc cgttctccct 630

<210> SEQ ID NO 119
<211> LENGTH: 1428
<212> TYPE: DNA
<213> ORGANISM: Oryza indica

<400> SEQUENCE: 119

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caaacctccc gtcgtgcttg gctgcggcgc cgtctccgcg gactacctcg ccaccgtcgc 180

ctccttcccc aaccccgacg acaagatccg aagcctaacg ctcaaggtcc agggaggcgg 240

caacactggc aatgccttga ccgccgctgc tcgtttgggc cttcgcccaa ggatcatatc 300

caaggtatcc aatgacccac aaggaagaaa tattctcaag gagctgcaag atgatggggt 360

cgacacctct catatcctgg ttgcagagga ggggaattca cctttcacct atataattgt 420

tgacaaccag acgaaaactc gtacttgtat tcacactcct ggttatcctc ctatggtccc 480

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tgatgtcaga ttgcatgaaa ctgctttact agttgctgaa gaggcaagcc aaagaaaact 600

tcctattttg attgatgccg aacggaagag ggatggattg gacgagcttc tcaatttcgc 660

atcttatgtt gtatgctctg caaaatttcc tcaggcttgg acaggagcct catcaacacc 720

ggttgctttg gtgtccatgc ttttaagatt gcctaatatc aagtttatta ttgtaaccct 780

tggagaaaag ggatgcttga tgcttgaaag aagcacaaca gatgcttctg aggcagagga 840

aatagatgta gagagtcttc tggaatcact agagaagaaa gaagttttga gttcaagcat 900

gccaaaatgc atcgcctcca agtcaaattt gagaataagt gcagatggaa taggatccat 960

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<212> TYPE: DNA
<213> ORGANISM: Oryza indica

<400> SEQUENCE: 120

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ctccttcccc aaccccgacg acaagatccg aagcctaacg ctcaaggtcc agggaggcgg 240

caacactggc aatgccttga ccgccgctgc tcgtttgggc cttcgcccaa ggatcatatc 300

caaggtatcc aatgacccac aaggaagaaa tattctcaag gagctgcaag atgatggggt 360

cgacacctct catatcctgg ttgcagagga ggggaattca cctttcacct atataattgt 420

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tgatgtcaga ttgcatgaaa ctgctttact agttgctgaa gaggcaagcc aaagaaaact 600

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ggttgctttg gtgtccatgc ttttaagatt gcctaatatc aagtttatta ttgtaaccct 780

tggagaaaag ggatgcttga tgcttgaaag aagcacaaca gatgcttctg aggcagagga 840

aatagatgta gagagtcttc tggaatcact agagaagaaa gaagttttga gttcaagcat 900

gccaaaatgc atcgcctcca agtcaaattt gagaataagt gcagatggaa taggatccat 960

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gcctgagaag atgctgcctt ttgcagctca agtggctgct tgcgggtgca ggggtttagg 1140

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ttggcttgtg ttaataagag agatttgtgt gctgttgttg caaggccc 1428

<210> SEQ ID NO 121
<211> LENGTH: 1172
<212> TYPE: DNA
<213> ORGANISM: Papaver rhoeas

<400> SEQUENCE: 121

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ttggaagagc agaaatccaa aaaccaaaat gacaaataag cttcagctga aaaagggaca 180

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ctagcagtga cagcagctgg aagaacagac tccttgtatt cgtcggtctg ttcatcatat    420

aattcccagg aaacaaatga aacaacccta actgcagttc cttccttcct gagctcacca    480

gcggcctttt cagcaatttc taattctgaa ccagtagcac acacgatgac atctggtttg    540

ttacctgtag agttgtctga tattgtgtaa cctcccttgg cgactccttc aatggaggtt    600

cctggaaggt ttgcaagctt ttgacgtgaa agggcaagaa ttgagggtct ctttctgttt    660

tcaactgcaa ccttgtatgc cccggcagtc tcgtttccgt cagcgggacg gaacataaga    720

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<210> SEQ ID NO 122
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<212> TYPE: DNA
<213> ORGANISM: Oryza japonica

<400> SEQUENCE: 122

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agcagaatac taaaattaaa gctacaacag gaagcttttt ggcttctaat attagctttg    180

ctcctcggcc tcagcctccg ctgccgcggc ctccctctct tccgcggctg ctgccatcag    240

ttcgtcaaat ttgtccgtct tgcccagcac tatttcaatc ttggctttct gcatagggcg    300

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cgagagctcc acttcgttat gcagctgcat gtacctcttg gcgaggttga cgtagaagaa    480

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ctcctccatg gccgccgccc gacgagtccc cgcggagcac cgtgcgcgag tgaaacggag    660

agcgcgaggc ggcgaagaag atgtggagga tttcggcggc gacggaggta agaggga       717
```

1. A method of creating a transfected or transgenic plant chosen from the group consisting of ornamental, horticultural, forestry, medicinal or Nicotiana sp. plants, exhibiting a dwarf phenotype comprising: expressing in the plant the DNA identified by a polynucleotide sequence chosen from the group consisting of SEQ. ID NO: 1-122 or the mRNA encoded by the DNA identified by a polynucleotide sequence chosen from the group consisting of SEQ. ID NO: 1-122:

2. A method of creating a transfected or transgenic plant chosen from the group consisting of ornamental, horticultural, forestry, medicinal or Nicotiana sp. plants, exhibiting a dwarf phenotype comprising the steps of:

(a) providing a viral inoculum capable of infecting a plant comprising the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122 or the mRNA encoded by the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122;

(b) applying said viral inoculum to a plant;

whereby the plant is infected and the DNA or the mRNA is expressed in the plant.

3. The method of claims **1** or **2** wherein the plant is turfgrass.

4. The method of claims **1** or **2** wherein the plant is fir tree.

5. A transfected or transgenic plant chosen from the group consisting of ornamental, horticultural, forestry, medicinal or Nicotiana sp. plants, exhibiting a dwarf phenotype made by the method comprising: expressing in the plant the DNA identified by a polynucleotide sequence chosen from the group consisting of SEQ. ID NO: 1-122 or the mRNA encoded by the DNA identified by a polynucleotide sequence chosen from the group consisting of SEQ. ID NO: 1-122.

6. The transfected or transgenic plant of claim 5 wherein the plant is turfgrass.

7. The transfected or transgenic plant of claim 5 wherein the plant is fir tree.

8. A transfected or transgenic plant chosen from the group consisting of ornamental, horticultural, forestry, medicinal or Nicotiana sp. plants, exhibiting a dwarf phenotype made by the method comprising the steps of:

(a) providing a viral inoculum capable of infecting a plant comprising the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122 or the mRNA encoded by the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122;

(b) applying said viral inoculum to a plant;

whereby the plant is infected and the DNA or the mRNA is expressed in the plant.

9. The transfected or transgenic plant of claim 8 wherein the plant is turfgrass.

10. The transfected or transgenic plant of claim 8 wherein the plant is fir tree.

11. A method of producing multiple crops of the plant of claims **5-10** comprising the steps of:

(a) planting a reproductive unit of the plant;

(b) growing the planted reproductive unit under natural light conditions;

(c) harvesting the plant; and

(d) repeating steps (a) through (c) at least once in the year.

12. A method of manufacturing a biopharmaceutical comprising:

(a) providing a plant that expresses a biopharmaceutical in the plant;

(b) providing a viral inoculum capable of infecting a plant comprising the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122 or the mRNA encoded by the DNA identified by a polynucleotide sequence chosen from the group of SEQ. ID NO: 1-122;

(c) applying said viral inoculum to the plant;

whereby the plant is infected, exhibits a dwarf phenotype, and expresses the biopharmaceutical.

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